

> 0 <  
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Quest - Quick User-directed Expression Search Tool  
Release 5.4

# -- Outline of search "claim36.plr" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "zara371.key".

Selected sequence key from "zara371.key":  
claim36 (AA) ID claim36 AA preliminary pattern

Followed by  
1 r or n or a or t or v  
2 f  
2 m or i or t or r or a or s  
2 r or h or e or c or s or d  
2 h or f or y  
2 w  
2 e or t or a or f or s  
2 g or q or t or a or d  
2 f or q or l

Selected files:

File : claim36.plr.pep

## -- Output Parameters --

Format Options: File Options:  
Nucleic acid code matching Exact Indirect file  
Find non-matching hits only No Sequence or key file  
Report key used Yes List of hits  
Note position of hit Yes Hit display  
Display full annotations Yes Name and annotations  
Sequence context 50 Yes

## -- Run Parameters --

Run mode Batch  
Time to start comparison now  
Notify at end of run No

1 match found in sequence:

s31612 ; TOIG of: s31612 check: 219 from: 1 to: 139  
(from "claim36.plr.pep")

TOIG of: s31612 check: 219 from: 1 to: 139

P1:S31612 - beta-1,3-glucanase homolog (clone A20) - rape (fragment)

C:Species: Brassica napus (rape)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Nov-2000

C:Accession: S31612

R:Hard, D.; Morrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.

submitted to the EMBL Data Library, December 1992

A:Description: The anther-specific protein encoded by the Brassica napus and

Arabidopsis thaliana A6 gene exhibits homology to beta-1,3-glucanases.

A:Reference number: S31612

A:Accession: S31612

A:Molecule type: mRNA

A:Residues: 1-139 <HIR>

A:Cross-references: EMBL:X69889; NID:G17733; PID:G17734

A:Experimental source: Clone A20

C:Superfamily: beta-1,3-glucanase

S31612 Length: 139 October 13, 2004 13:40 Type: P Check: 219  
Found using 'claim36' (zara371.key)

49 WCVAVGANETELGALDFACGRSNATCALAPGECYAPVSTWHSYAFSSYWAQFR 99 107

109 NQSSQCYFNGLARETTTNPNGNCKFPSTVL

1 match found in sequence:  
s74688 ; TOIG of: s74688 check: 9387 from: 1 to: 391  
(from "claim36.plr.pep")

TOIG of: s74688 check: 9387 from: 1 to: 391

P1:S74688 - hypothetical protein s111200 - Synchocystis sp. (strain PCC 6803)

C:Species: Synchocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999

C:Accession: S74688

R:Kaneko, T.; Sato, S.; Korani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;

Miyajima, N.; Hirosewa, M.; Sugita, M.; Sasamoto, S.; Kimura, T.; Hosouchi,

T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpou, S.;

Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium

Synchocystis sp. PCC6803. II. Sequence determination of the entire genome and

assignment of potential protein-coding regions.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74688

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-391 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:G1651897; PID:BAAL6839.1;

PID:D1017572; PID:G1651913

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June

1996

S74688 Length: 391 October 13, 2004 13:40 Type: P Check: 9387

Found using 'claim36' (zara371.key)

## -- Search Statistics --

Times: CPU Total Elapsed  
00:00:00.00 00:00:00.00

Number of sequences searched: 2  
Number of sequence hits: 2  
Number of separate matches: 2  
Number of sequence hits saved: 0

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> O <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "claim36\_uni" --

Selected search type is key against sequence data banks or files.  
Selected scope is Sequence.

Selected sequence key from "zara371.key":

claim36 (AA) ID claim36 AA preliminary pattern  
followed by  
1 r or n or a or t or v  
2 f  
2 m or l or t or r or a or s  
2 r or h or e or c or s or d  
2 h or f or y  
2 w  
2 e or t or a or f or s  
2 g or q or t or a or d  
2 f or q or l

Selected files:

File : claim36uni.pep

-- Output Parameters --

Format Options:	File Options:	
Nucleic acid code matching	Indirect file	NO
Find non-matching hits only	Sequence or key file	NO
Report key used	List of hits	YES
Note position of hit	Hit display	YES
Display full annotations	Name and annotations	YES
Sequence context		50

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	NO

1 match found in sequence:

aaq23617 ; LD10322P.

(from "claim36uni.pep")

TOIG of: aaq23617 check: 1097 from: 1 to: 1075

ID	AAQ23617	PRELIMINARY;	PRT;	1075 AA.
AC	AAQ23617;			
DT	02-MAR-2004 (TrEMBLrel. 27, Created)			
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)			
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)			
DE	LD10322P.			
GN	CG16718.			
OS	Drosophila melanogaster (fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Berkley;			
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,			
RA	Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fritse E.,			
RA	George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,			
RA	Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,			
RA	Patel S., Phouneavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,			
RA	Celniker S.;			
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.			

DR EMBL; BF010299; AAQ23617.1; -;  
SQ SEQUENCE 1075 AA; 123934 MW; 729765FBD8339C70 CRC64;

AAQ23617 Length: 1075 October 13, 2004 13:25 Type: P Check: 1097  
Found using 'claim36' (zara371.key)

...

451 VPKKDTCQSGNTITMCPCLCDMGNFMDLKETCNVAKTYLIDNPSTVFPAVFPMTLP  
501 509

511 LELWKRSAREITHRWDLTGFDVHEHPRPOLARLEHIPTPRVDYVTNI

...

1 match found in sequence:

aaq72537 ; SCL-PHA synthase.

(from "claim36uni.pep")

TOIG of: aaq72537 check: 4418 from: 1 to: 566

ID	AAQ72537	PRELIMINARY;	PRT;	566 AA.
AC	AAQ72537;			
DT	02-MAR-2004 (TrEMBLrel. 27, Created)			
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)			
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)			
DE	SCL-PHA synthase.			
GN	PHAC.			
OS	Pseudomonas sp. HJ-2.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OC	Pseudomonadaceae; Pseudomonas.			
OX	NCBI_TaxID=244327;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HJ-2;			
RA	Seo S.H., Choi G.G., Rhee Y.H.;			
RT	"Cloning of scl-pHA synthase locus and mcl-pHA synthase locus in			
RT	Pseudomonas sp. HJ-2."			
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY370931; AAQ72537.1; -;			
SQ	SEQUENCE 566 AA; 63672 MW; F4CBA744CE5943F0 CRC64;			
AAQ72537	Length: 566 October 13, 2004 13:25 Type: P Check: 4418			
Found using 'claim36' (zara371.key)				
1	MDNGHTFAHWSCQAPFIASFVLQQLRLVVAQNTWFSGHDSQMFDPVBEALQLQADYQ			
6	14			
61	QQWA			
...				
1 match found in sequence:				
caea45695 ; Hypothetical protein.				
(from "claim36uni.pep")				
TOIG of: caea45695 check: 6871 from: 1 to: 180				
ID	CAB45695	PRELIMINARY;	PRT;	180 AA.
AC	CAB45695;			
DT	02-MAR-2004 (TrEMBLrel. 27, Created)			
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)			
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Streptomyces parvulus.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycineae; Streptomycetaceae; Streptomycetes.			
OX	NCBI_TaxID=146923;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TV4055;			

RA Olano C., Wilkinson B., Sanchez C., Moss S., Sheridan R., Math V.,  
 RA Weston A.J., Brana A.F., Martin C., J., Oilynyk M., Mendez C.,  
 RA Leadlay P.F., Salas J.A.;  
 RT "Biosynthesis of the angiotensin inhibitor borrelidin by Streptomyces  
 RT parvulus Tu4055: cluster analysis and assignment of functions.";  
 RL Chem. Biol. 11:87-97(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tu4055;  
 RA Olano C., Wilkinson B., Moss S., Brana A.F., Mendez C., Leadlay P.F.,  
 RA Salas J.A.;  
 RT "Evidence from engineered gene fusions for the repeated use of a  
 RT module in a modular polypeptide synthase";  
 RL Chem. Commun. 22:2780-2782(2003).  
 DR EMBL; AJ580915; CAB45695.1; -;  
 KW Aminotransferase; Hypothetical protein; Oxidoreductase.  
 SQ SEQUENCE 180 AA; 19338 MW; 6CCE28A1E48436DB CRC64;  
 CAB45695 Length: 180 October 13, 2004 13:25 Type: P Check: 6871 ..  
 Found using 'claim36' (zara371.key)  
 ...  
 7 EAAKVELVPSLFDANGNGVYDSDPDMLTDRVVAAGSDSAAKAAVRAAFRRYTTTLA  
 57  
 65  
 67 TELDAGDGVIVEEFRFPVLDPERFGPTIAEFARALSAIDPDGDLI  
 -----  
 1 match found in sequence:  
 P72824 ; S11200 protein.  
 (from "claim36uni.pep")  
 TOIG of: p72824 check: 9387 from: 1 to: 391  
 ...  
 ID P72824 PRELIMINARY; PRT; 391 AA.  
 AC P72824;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE S11200 protein.  
 GN OrderedLocustNames=S11200; PCC 6803).  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 RA Sugita M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 RT region from map positions 644 to 924 of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC6803;  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nartou K., Okumura S.,  
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL; D90901; BAA16839.1; -;  
 DR PIR; S74688; S74688.  
 KW Complete proteome.  
 SQ SEQUENCE 391 AA; 42240 MW; 1AFDB350FDEDD2A45 CRC64;

P72824 Length: 391 October 13, 2004 13:25 Type: P Check: 9387 ..  
 Found using 'claim36' (zara371.key)  
 ...  
 296 FWLPAIAFSWLLGSSILNGLIPLLLEILQNGQGVIGLYGFCVGLADVFTRWSTOS  
 346  
 354  
 356 SQMHGGLGLMLVMSITLLCARVWQGFVFNKKGAGD  
 -----  
 1 match found in sequence:  
 q06913 ; Beta-1,3-glucanase homologue (Fragment).  
 (from "claim36uni.pep")  
 TOIG of: q06913 check: 219 from: 1 to: 139  
 ...  
 ID 006913 PRELIMINARY; PRT; 139 AA.  
 AC 006913;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Beta-1,3-glucanase homologue (Fragment).  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroside II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94108487; PubMed=8281185;  
 RA Hard D.L., Worrall D., Hodge R., Smart S., Paul W., Scott R.;  
 RT "The anther-specific protein encoded by the Brassica napus and  
 RT Arabidopsis thaliana A6 gene displays similarity to beta-1,3-  
 RT glucanases.";  
 RL Plant J. 4:1023-1033(1993).  
 DR EMBL; X69889; CAA49515.1; -;  
 DR PIR; S31612; S31612.  
 DR GO; GO:0004553; Phosphatase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; Polysaccharide metabolism; IEA.  
 DR InterPro: IPR000480; Glyco\_hydro\_17.  
 DR Pfam: PF00332; Glyco\_hydro\_17; 1.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 139 AA; 14995 MW; ECBBD6335C551F7 CRC64;  
 006913 Length: 139 October 13, 2004 13:25 Type: P Check: 219 ..  
 Found using 'claim36' (zara371.key)  
 ...  
 49 VMCVAVEGANETELGQALDPACGRSNATCAALAPGRECVAPSVTWHAASYAFSSVAOFR  
 99  
 107  
 109 NQSSQCYFNGLARLETTTNPENBOCKFPSVTL  
 -----  
 1 match found in sequence:  
 q6ufw5 ; SCL-PHA synthase.  
 (from "claim36uni.pep")  
 TOIG of: q6ufw5 check: 4418 from: 1 to: 566  
 ...  
 ID 06UFW5 PRELIMINARY; PRT; 566 AA.  
 AC 06UFW5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE SCL-PHA synthase.  
 GN Name=phac;  
 OS Pseudomonas sp. HJ-2.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.

OX NCBI\_TaxId=244327;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HJ-2.  
RA Seo S.H., Choi G.G., Rhee Y.H.,  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY370931; AAQ72537.1; -  
DR InterPro; IPR000073; A/b hydrolase.  
DR InterPro; IPR010941; Phac\_N.  
DR InterPro; IPR010963; PhA\_synth\_I.  
DR Pfam; PF00561; Abhydrolase\_1; 1.  
DR Pfam; PF07167; Phac\_N; 1.  
DR TIGRfam; TIGR01838; PhA synth I; 1.  
SQ SEQUENCE 566 AA; 63672 MW; F4CBA74ACE5943F0 CRC64;

QGUF5 Length: 566 October 13, 2004 13:25 Type: P Check: 4418 ..  
Found using 'claim36' (zara371.key)

1 MDNGHFAHYWSGOAPRIASFVLQQLRYVAQNTWFGSDQSGWFDVPEALBQLQADYQ  
6 14

61 QQWA

1 match found in sequence:  
q70hx4 ; Hypothetical protein.  
(from "claim36un1.pep")  
TOIG of: q70hx4 check: 6871 from: 1 to: 180

ID Q70HX4 PRELIMINARY; PRT; 180 AA.  
AC Q70HX4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
OS Hypothetical protein.  
OC Streptomyces parvulus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxId=146923;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Tu4055;  
RX PubMed=15113998;  
RA Olanco C., Wilkinson B., Sanchez C., Moss S., Sheridan R., Math V.,  
RA Weston A.J., Brana A.F., Martin C., J., Olinyk M., Mendez C.,  
RA Leadlay P.F., Salas J.A.;  
RT "Bioynthesis of the anglogenesis inhibitor borrelidin by Streptomyces  
parvulus Tu4055: cluster analysis and assignment of functions.";  
RL Chem. Biol. 11:87-97(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Tu4055;  
RA Olanco C., Wilkinson B., Moss S., Brana A.F., Mendez C., Leadlay P.F.,  
RA Salas J.A.;  
RT "Evidence from engineered gene fusions for the repeated use of a  
module in a modular polypeptide synthase";  
RL Chem. Commun. 22:2780-2782(2003).  
DR EMBL; AJ580915; CA645695.1; -  
DR InterPro; IPR002048; EF-hand  
DR InterPro; IPR010983; EF\_Hand\_Like.  
DR Pfam; PF00036; efhand; 3.  
DR SMART; SM00054; Efn; 3.  
DR PROSITE; PS00018; EF\_HAND; 2.  
KM Calcium-binding; Hypothetical protein.  
SQ SEQUENCE 180 AA; 19338 MW; 6CCE88A1E4836DB CRC64;

Q70HX4 Length: 180 October 13, 2004 13:25 Type: P Check: 6871 ..  
Found using 'claim36' (zara371.key)

7 EAKRVELVPSLFDANGNGVIDSDDFDLMTRVAAAAGSDSAAKAAVAPRRYTTTLA  
57 65

67 TELDADGGVITVEERRPFVLDPERFGPTIAEPARALSAIGDGDGLI

1 match found in sequence:  
q7mgv7 ; Sensor histidine kinase.  
(from "claim36un1.pep")  
TOIG of: q7mgv7 check: 6631 from: 1 to: 1156

ID Q7MGU7 PRELIMINARY; PRT; 1156 AA.  
AC Q7MGU7;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Sensor histidine kinase.  
GN Name=V3129;  
OS Vibrio vulnificus (strain V316).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxId=196600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14656965;  
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,  
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,  
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;  
RT "Comparative genome analysis of Vibrio vulnificus, a marine  
pathogen";  
RT Genom. Res. 13:2577-2587(2003).  
RL CC  
CC -1- SIMILARITY: Contains 1 histidine kinase domain.  
DR EMBL; AP005342; BAC95893.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0000156; F:two-component response regulator activity; IEA.  
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.  
DR InterPro; IPR003594; ATPbind\_Atpase.  
DR InterPro; IPR004358; Bact\_sens\_pr\_C.  
DR InterPro; IPR005467; His\_Kinase.  
DR InterPro; IPR003661; His\_Kinase\_N.  
DR InterPro; IPR001734; Na/Solut\_symp.  
DR InterPro; IPR001789; Response\_reg.  
DR Pfam; PF02518; HATPase\_C; 1.  
DR Pfam; PF00512; HisKA; 1.  
DR PRINTS; PR00344; BCTRUSENSOR.  
DR PRODOM; PD000039; Response\_reg; 1.  
DR PROSITE; PS50109; HIS\_KIN; 1.  
DR PROSITE; PS50283; NA\_SOLUT\_symp\_3; 1.  
DR PROSITE; PS50110; RESPONSE\_REGULATORY; 1.  
KM Kinase; Phosphorylation; Sensory transduction; Transferase.  
SQ SEQUENCE 1156 AA; 128283 MW; 4DB3AB41A0B1A4FB CRC64;

Q7MGU7 Length: 1156 October 13, 2004 13:25 Type: P Check: 6631 ..  
Found using 'claim36' (zara371.key)

518 PLSERLQSHAFVGTPLPENENISLYQSRVTGELMLASRFVGNRRVKNAPAHYWSQR  
568 576

578 ETLPNQQAESTLIRHTEVLAGVFGASSAKLVLTSLAQGRNMQLEVA

```

1 match found in sequence:
q86p24 ; RE22501p (Fragment).
  (from "claim36uni.pep")
TOIG of: q86p24 check: 8357 from: 1 to: 972

ID 086P24 PRELIMINARY; PRT; 972 AA.
AC 086P24;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE RE22501p (Fragment).
GN ORFNames=CG16718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dreesnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guartin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Munco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT003522; AAC039526.1; -
DR FlyBase; FBgn0038721; CG16718.
DR InterPro; IPR007632; DUF590.
DR Pfam; PF04547; DUF590; 1.
FT NON_TER
SQ SEQUENCE 972 AA; 112363 MW; 57DF924CFD245843 CRC64;

Q86P24 Length: 972 October 13, 2004 13:25 Type: P Check: 8357
Found using 'claim36' (zara371.key)

...

348 VPKYKICQSGNTNITWCPICDWCNFWDLKETCNAYKVTYLLDNPSVTFVAFVMSFWATLP
|-----|
408 LELMKRYASBITHRMDLTGDFVHEHPRFOYLARLEHIPTRVDTYVNI 398 406

1 match found in sequence:
q86c25 ; Signal transduction histidine kinase.
  (from "claim36uni.pep")
TOIG of: q86c25 check: 2146 from: 1 to: 1143

ID 08DC25 PRELIMINARY; PRT; 1143 AA.
AC 08DC25;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Signal transduction histidine kinase.
GN OrderedLocusNames=V11242;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_Taxid=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;

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RT RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AE016801; AAC09698.1; -
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR011006; CheY_like.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR009082; His_kin_homodim.
DR InterPro; IPR001734; Na/golult_sympot.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HisKA; 1.
DR Pfam; PF00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PSS0109; HIS_KIN; 1.
DR PROSITE; PSS0283; NA_SOLUT_SYMP_3; 1.
DR PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
KW transference.
SQ SEQUENCE 1143 AA; 126643 MW; 85F47E27E3B2D621 CRC64;

Q8DC25 Length: 1143 October 13, 2004 13:25 Type: P Check: 2146
Found using 'claim36' (zara371.key)

...

505 PLSIERLQASPFVGTPLPENENISLYQSRVTYGELEMLASRFVGRNRVKNAPFAHWVSOOR
|-----|
565 ETLIPNOQAPSTLIRHTERVLAVFGASAKLVLTSLAGRMQLLEVA 555 563

1 match found in sequence:
q8in71 ; CG16718-PB.
  (from "claim36uni.pep")
TOIG of: q8in71 check: 3404 from: 1 to: 926

ID 08IN71 PRELIMINARY; PRT; 926 AA.
AC 08IN71;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CG16718-PB.
GN ORFNames=CG16718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20196006; PubMed=10731112;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champs M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
 RA Abri J.F., Abgaryan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,  
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostreli A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [12]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=2242605; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champs M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 RT melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [13]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [14]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22426069; PubMed=12537572;  
 RA Miya S., Crosby M.A., Mungall C.U., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [15]  
 RP SEQUENCE FROM N.A.  
 RG FLYBASE:  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [16]  
 RN SEQUENCE FROM N.A.  
 RG FLYBASE:  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A0003727; A0013804.1; -;  
 DR FlyBase; Fggn0038721; CG16718.  
 DR InterPro; IPR007632; DUF590.  
 DR Pfam; PF04547; DUF590.1.  
 SQ SEQUENCE 926 AA; 107585 MW; 1F33F7DDEAE07368 CRC64;  
 Q01N71 Length: 926 October 13, 2004 13:25 Type: P Check: 3404  
 Found using 'claim36' (zara371.key)  
 ...  
 302 VPKYKDCSGSNNITMCPICDMCNFMDKETCNVATYVLIDNPSTVFAVPSFATLTF  
 352  
 360  
 362 LELMKRYSAEITHRMDLTGFDVHEEHPPOYLARLEHIPTRVYVYNNI  
 ...  
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 1 match found in sequence:  
 q81b06 ; Putative glucan endo-1-3-beta-glucosidase.  
 (from "claim36\_uni.pep")  
 TOIG of: q81b06 check: 8289 from: 1 to: 460  
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 ID Q81B06 PRELIMINARY; PRT; 460 AA.  
 AC Q81B06;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative glucan endo-1-3-beta-glucosidase.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation.";  
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY087496; AAM65039.1; -;  
 DR HSSP; P12257; IAO.  
 DR GO; GO:0004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000490; Glyco\_hydro\_17.  
 DR Pfam; PF00332; Glyco\_hydro\_17; 1.  
 DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; UNKNOWN 1.  
 SQ SEQUENCE 460 AA; 50643 MW; DF336100601162C CRC64;  
 Q81B06 Length: 460 October 13, 2004 13:25 Type: P Check: 8289  
 Found using 'claim36' (zara371.key)  
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 370 IMCVAKGNMTQGLDALSYACSGSNNITCDPIRGSGPCKKPDLTVLHASYAVSSVYAGFR

430 KIGTCSFNGLATGRIKIDPSYGRCEPSSVTL

420 428

1 match found in sequence:

g91b4 ; Beta-1,3-glucanase, putative.  
(from "claim36uni.pep")

TOIG of: g91b4 check: 2648 from: 1 to: 476

ID Q91B4 PRELIMINARY; PRT; 476 AA.  
AC Q91B4;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)  
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE Beta-1,3-glucanase, putative.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP MEDLINE=2208475; PubMed=12093376;  
RA Haas B.-J., Volkov N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RT annotation.";  
RT Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY086926; AAM64490.1; -  
DR HSSP; P15737; IGHS.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000490; Glyco\_hydro\_17.  
DR InterPro; IPR01050; Pectin\_lyas\_1like.  
DR Pfam; PF00332; Glyco\_hydro\_17; 1  
DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; UNKNOWN\_1.  
SQ SEQUENCE 476 AA; 52087 MW; 22DEBA17FA96B3 CRC64;

Q91B4 Length: 476 October 13, 2004 13:25 Type: P Check: 2648 ..  
Found using 'claim36' (zara371.key)

386 WCVAVDGADEAEALGQALNFCGRSNATCALAPGGEYAPVTWTHASVAFSSWAQFR  
436 444

446 NOSQCYFNGLARETTTPGNERCKEPPSVTL

1 match found in sequence:

g91k41 ; Beta-1,3-glucanase.  
(from "claim36uni.pep")

TOIG of: g91k41 check: 2170 from: 1 to: 476

ID Q91K41 PRELIMINARY; PRT; 476 AA.  
AC Q91K41;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE Beta-1,3-glucanase.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20363099; PubMed=10907853;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.  
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,  
RT TAC and BAC clones.";  
RT DNA Res. 7:217-221(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP000377; BAB01853.1; -  
DR HSSP; P15737; IGHS.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000490; Glyco\_hydro\_17.  
DR Pfam; PF00332; Glyco\_hydro\_17; 1  
DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; UNKNOWN\_1.  
SQ SEQUENCE 476 AA; 52170 MW; 9B36D1BA6109B46E CRC64;

Q91K41 Length: 476 October 13, 2004 13:25 Type: P Check: 2170 ..  
Found using 'claim36' (zara371.key)

386 WCVAVDGADEAEALGQALNFCGRSNATCALAPGGEYAPVTWTHASVAFSSWAQFR  
436 444

446 NOSQCYFNGLARETTTPGNERCKEPPSVTL

1 match found in sequence:

g9sfw1 ; Putative beta-1,3-glucanase.  
(from "claim36uni.pep")

TOIG of: g9sfw1 check: 9732 from: 1 to: 440

ID Q9SFW1 PRELIMINARY; PRT; 440 AA.  
AC Q9SFW1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE Putative beta-1,3-glucanase.  
GN Name=T1B9.1;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,  
RA Roming C.M., Koo H., Fujii C.Y., Utebbeck T.R., Barnstead M.E.,  
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC012395; AAF20214.1; -  
DR HSSP; P12257; IAOO.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000490; Glyco\_hydro\_17.  
DR Pfam; PF00332; Glyco\_hydro\_17; 1  
DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; UNKNOWN\_1.  
SQ SEQUENCE 440 AA; 48538 MW; FC8B6A3B34B8D93 CRC64;

Q9SFW1 Length: 440 October 13, 2004 13:25 Type: P Check: 9732 ..  
Found using 'claim36' (zara371.key)

350 KTEYKESLPAPENNDLKYGKICVGNNTCDPIORGSPCKPDLTVLHNASVAFSSWAQFR  
400 408



410 KIGTCSFNGLATOTIKDPSYGRCEPSPVTL

1 match found in sequence:

g9vdt4 ; Putative glucan endo-1-3-beta-glucosidase (Putative beta-1,3-  
 (from "claim36uni.pep")  
 TOIG of: g9srt4 check: 8766 from: 1 to: 460

ID Q9SRT4 PRELIMINARY; PRT; 460 AA.  
 AC Q9SRT4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative glucan endo-1-3-beta-glucosidase (Putative beta-1,3-  
 glucanase) (Putative glycosyl hydrolase)  
 GN Name=F2103.3; Synonym=At3g07320, At3g07320/t1b9\_1;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxId=702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,  
 RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,  
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A0009853; AAF02143.1; -  
 DR EMBL: AK118068; BAC4269.1; -  
 DR EMBL: BT005678; AA064098.1; -  
 DR HSSP: P12257; 1A00.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR000490; Glyco\_Hydro\_17.  
 DR Pfam: PF00332; Glyco\_Hydro\_17; 1.  
 DR PROSITE: PS00587; GLYCOSYL\_HYDROL\_F17; UNKNOWN\_1.  
 KW Hydrolase.  
 SQ SEQUENCE 460 AA; 50603 MW; D2061EAA09C085F CRC64;

Q9SRT4 Length: 460 October 13, 2004 13:25 Type: P Check: 8766  
 Found using 'claim36' (zara371.key)

430 KIGTCSFNGLATOTIKDPSYGRCEPSPVTL

370 IWCVAKGANWTLGDLALSYACSGQGNNTCDPIORGPCQKPDLTLYHASYAFSPSYAQR

420 428

1 match found in sequence:  
 g9vdt4 ; CG16718-PA (LD10322p).  
 (from "claim36uni.pep")  
 TOIG of: g9vdt4 check: 1097 from: 1 to: 1075

ID G9VDV4 PRELIMINARY; PRT; 1075 AA.  
 AC G9VDV4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CG16718-PA (LD10322p).  
 GN ORFNAMES=CG16718;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.T., Andrews-Planck C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostali D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Liang Y., Lin X.,  
 RA Laske P., Lei Y., Levitsky A.A., Li Z., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nuskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Munz D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sedgeman E.J.,  
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22426070; PubMed=12537573;  
 RA Kamincher J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 a genomic perspective.";

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RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Croebly M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Beltenkourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesnek D., Farfan D., Frise B.,
RA George R., Gonzalez M., Guartin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Munco J., Paclob J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
RA Celinker S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003727; AAF55685.1; -
DR EMBL; BT010299; AAQ23617.1; -
DR Inact: Q9VDV4; -
DR FlyBase; FBgn0038721; CG16718.
DR InterPro; IPR007632; DUF590.
DR Pfam; PF04547; DUF590; 1.
SQ SEQUENCE 1075 AA; 123934 MW; 729765FBD8339C70 CRC64;

O9VDV4 Length: 1075 October 13, 2004 13:25 Type: P Check: 1097 ..
Found using 'claim36' (zara371.key)

...

451 VPKDICSQNTNITWCPICDWCNFWDLKETCNVAKVTYLIDNPSTVFPFAVWSPWATLFP
|-----|
501 509

511 LELWKRYSAEITHRWDLTGFDVHEHHPPOYLARLEHIPPTRVDVYVNI

...

-- Search Statistics --

Times: CPU Total Elapsed
00:00:00.00 00:00:00.00

Number of sequences searched: 17
Number of sequence hits: 17
Number of separate matches: 17
Number of sequence hits saved: 0

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> O <  
O | O Intelligenetics  
> O <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "claim36\_spt" --

Selected search type is key against sequence data banks or files.  
Selected scope is Sequence.

Selected sequence key from "zara371.key":

claim36 (AA) ID claim36 AA preliminary pattern

followed by

1 r or n or a or t or v  
2 f  
2 m or l or t or r or a or s  
2 r or h or e or c or s or d  
2 h or f or y  
2 w  
2 e or t or a or f or s  
2 g or q or t or a or d  
2 f or q or l

Selected files:

File : claim36spt.pep

-- Output Parameters --

Format Options:

Nucleic acid code matching Exact  
Find non-matching hits only No  
Report key used Yes  
Note position of hit Yes  
Display full annotations Yes  
Sequence context 50

File Options:

Indirect file  
Sequence or key file  
List of hits  
Hit display  
Name and annotations  
Yes  
Yes  
Yes  
Yes

-- Run Parameters --

Run mode Batch  
Time to start comparison now  
Notify at end of run No

1 match found in sequence:

p72824 ; Hypothetical protein s111200.  
(from "claim36spt.pep")

TOIG of: p72824 check: 9387 from: 1 to: 391

ID P72824 PRELIMINARY; PRT; 391 AA.  
AC P72824;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein s111200.  
GN SL11200.  
OS Synchocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97061201; PubMed=8905231;  
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraiki A., Nakazaki N., Nartuo K., Okumura S.,  
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
RA Tabata S.,  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).

DR EMBL; D90901; BAA16839.1; --  
DR PIR; S74688; S74688.  
DR InterPro; IPR007110; Ig-like.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 391 AA; 42240 MW; 1AFDB350FDEBD2A5 CRC64;  
P72824 Length: 391 October 13, 2004 13:38 Type: P Check: 9387  
Found using 'claim36' (zara371.key)

296 FWLPAIAFWLIGSSILNGLIPLEIILIQNGTGVIGLPGCVGIAGDPVFTFRWSTOS  
346 354

356 SQMHGIGLGLAMLVMSITLLCARYWQGRVPPKKGAGD

1 match found in sequence:

q06913 ; Beta-1,3-glucanase homologue (Fragment).  
(from "claim36spt.pep")

TOIG of: q06913 check: 219 from: 1 to: 139

ID Q06913 PRELIMINARY; PRT; 139 AA.  
AC Q06913;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Beta-1,3-glucanase homologue (Fragment).  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3706;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94108487; PubMed=8281185;  
RA Hird D.L., Morrall D., Hodge R., Smart S., Paul W., Scott R.;  
RT "The anther-specific protein encoded by the Brassica napus and  
RT Arabidopsis thaliana A6 gene displays similarity to beta-1,3-  
RT glucanases.";  
RT Plant J. 4:1023-1033(1993).  
DR EMBL; X69889; CAA49515.1; --  
DR PIR; S31612; S31612.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000490; Glyco\_hydro\_17.  
DR Pfam; PF00332; Glyco\_hydro\_17; 1.  
FT NON TER 1  
SQ SEQUENCE 139 AA; 14995 MW; ECBBD6335C551F7 CRC64;  
Q06913 Length: 139 October 13, 2004 13:38 Type: P Check: 219  
Found using 'claim36' (zara371.key)

49 VMCVAVEGANETELGQALDPACGRSNATCAALAPGECYAPVSVTWASYSYNAQER  
99 107

109 NQSSQCYFNGIARETTTTPNGNEQKFPVSVL

1 match found in sequence:

q86p24 ; RE2501P (Fragment).  
(from "claim36spt.pep")

TOIG of: q86p24 check: 8357 from: 1 to: 972

ID Q86p24 PRELIMINARY; PRT; 972 AA.  
AC Q86p24;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE RE22501p (Fragment).
GN CG16718.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Stapleton M., Brockstein P., Hong L., Agbayan A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dyesnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Munro J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT003522; AA039526.1; -.
DR InterPro; IPR007632; DUF590.
DR Pfam; PF04547; DUF590; 1.
DR NON TER 1 1.
SQ SEQUENCE 972 AA; 112363 MW; 57DF924CFD245843 CRC64;

Q86P24 Length: 972 October 13, 2004 13:38 Type: P Check: 8357
Found using 'claim36' (zara371.key)

...

348 VPKDICQSGNNTITMCP.LCDMCNFWDKETCNVATYVILIDNPSTVFPAVENSFATLTF
|-----|
398 406

408 LELMKRYSAEITHRMDLTGFDVHEHRRPQYARLEHIPPTRVDVYVNTI

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1 match found in sequence:
q8dc25 ; Signal transduction histidine kinase.
(from "claim36spt.pep")
TOIG of: q8dc25 check: 2146 from: 1 to: 1143

ID Q8DC25 PRELIMINARY; PRT; 1143 AA.
AC Q8DC25;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Signal transduction histidine kinase.
GN V11242.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE016801; AA009698.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0006160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR005467; His_kinase.

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DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR001734; Na/biol_sympor.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c1.
DR Pfam; PF00512; HATPase_c1.
DR Pfam; PF00072; response_reg.1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg.1.
DR SMART; SM00387; HATPase_c1.
DR SMART; SM00448; REC.1.
DR SMART; SM00409; His_KIN.1.
DR PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY.1.
KW Kinase; Complete proteome.
SQ SEQUENCE 1143 AA; 126643 MW; 85F47E27E3B2D621 CRC64;

Q8DC25 Length: 1143 October 13, 2004 13:38 Type: P Check: 2146
Found using 'claim36' (zara371.key)

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505 PLSISERLQSGASFVGTPLPENENISLYQSRVWGELEMLASRFVGRNRVNAFAHWYSQSR
|-----|
555 563

565 ETLPLNQAPSTLIRHTRERVLAVFGASGSAKVLTSALQGRNMQLLEVA

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1 match found in sequence:
q8in71 ; CG16718-PB.
(from "claim36spt.pep")
TOIG of: q8in71 check: 3404 from: 1 to: 926

ID Q8IN71 PRELIMINARY; PRT; 926 AA.
AC Q8IN71;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG16718-PB.
GN CG16718.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abril J.F., Agbayan A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck U., Brokstein P., Brotlier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.U., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glisick A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA  Liu X.G., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merklov G., Milbina N.V., Mobbart C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
RA  Palazolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.Y., Waasatman D.A., Weinstein G.M., Weissbach J.,
RA  Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA  Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA  Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA  Banazon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA  Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA  Dodson K., Dorssett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA  Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA  Gonzales M., Houck J., Hoekins R.A., Hostin D., Howland T.J.,
RA  Ibegwam C., Jatali M., Kruse D., Li P., Matzel B., Moshrefi A.,
RA  McInosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA  Pacleb J., Parasas V., Park S., Patel S., Pfeiffer B.,
RA  Phounenavong S., Piltman G.S., Puri V., Richards S., Scheeler F.,
RA  Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA  Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT  "Sequencing of Drosophila melanogaster genome.";
RN  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL  [3]
RP  SEQUENCE FROM N.A.
RA  Miers S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA  Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA  Tupy J.L., Bergman C., Bernat B., Carlson J.W., Celniker S.E.,
RA  Clamp W., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA  Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA  Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA  Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT  "Annotation of Drosophila melanogaster genome.";
RN  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL  [4]
RP  SEQUENCE FROM N.A.
RA  Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN  [5]
RP  SEQUENCE FROM N.A.
RA  FlyBase;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL, AB003727; AANJ3804.1; -
DR  FlyBase; FBgn0038721; CG16718.
DR  InterPro; IPR007632; DUF590.
DR  Pfam; PF04547; DUF590; 1.
SQ  SEQUENCE 926 AA; 107585 MW; 1F33F7DDEAE07368 CRC64;

OBIN1. length: 926 October 13, 2004 13:38 Type: P Check: 3404 ..
Found using 'claim36' (zara371.key)

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q81b06 ; Putative glucan endo-1,3-beta-glucosidase.
(from "claim36pt.pep")
TOIG of: q81b06 check: 8289 from: 1 to: 460

ID Q81B06 PRELIMINARY; PRT; 460 AA.
AC Q81B06;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative glucan endo-1,3-beta-glucosidase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxId=3702;
RX [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troupkhan M., Alexandrov N.,
RA Felmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Felmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087496; AAM65039.1;
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000490; Glyco_hydro_17.
DR Pfam; PF00332; Glyco_hydro_17.1.
DR PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
SQ SEQUENCE 460 AA; 50643 MW; DF33610060162C CRC64;

Q81B06 Length: 460 October 13, 2004 13:38 Type: P Check: 8289
Found using 'Claim36' (zar3371.key)

...

370 INCVAKAGNMTQLGDLALSYACSGNNTCDPIQRGFCQKRDLTVLHASYAFSSYMAQFR
420 428

370 KIGCTCSFNGLATQTITKDPYSYRCFPESVTL

430

-----
1 match found in sequence:
q81b04 ; Beta-1,3-glucanase, putative.
(from "claim36pt.pep")
TOIG of: q81b04 check: 2648 from: 1 to: 476

ID Q81B04 PRELIMINARY; PRT; 476 AA.
AC Q81B04;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-1,3-glucanase, putative.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxId=3702;
RX [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troupkhan M., Alexandrov N.,
RA Felmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavel R.,  
 RA Feldmann K.;  
 RT "Full-length cDNA from Arabidopsis thaliana."  
 RU Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY066926; AAM64490.1; -  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000490; Glyco\_hydro\_17.  
 DR Pfam; PF00332; Glyco\_hydro\_17; 1.  
 DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; 1.  
 SQ SEQUENCE 476 AA; 52087 MW; 22DDEEA17FA96EB3 CRC64;  
 Q8LBV4 Length: 476 October 13, 2004 13:38 Type: P Check: 2648  
 Found using 'claim36' (zara371.key)

386 WVCVAVDGADEALGQALNPFACGRSNATCALAPGEGYAPVTVTWHSYATSSYWAQFR  
 436 444

446 NOSOCYFNGLARETTTPGNERCKEPPSVTL

-----  
 1 match found in sequence:  
 g91k41; Beta-1,3-glucanase.  
 (from "claim36spt.pep")  
 TOIG of: g91k41 check: 2170 from: 1 to: 476

ID Q9LK41 PRELIMINARY; PRT; 476 AA.  
 AC Q9LK41;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Beta-1,3-glucanase.  
 OS Arabidopsis thaliana (Mouse-ear cress);  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=20363099; PubMed=10907853;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.  
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,  
 RT TAC and BAC clones."  
 RT DNA Res. 7:217-221(2000).  
 RL EMBL; AP000377; BAB01853.1; -  
 DR HSSP; P15737; IGHS.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000490; Glyco\_hydro\_17.  
 DR Pfam; PF00332; Glyco\_hydro\_17; 1.  
 DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; 1.  
 SQ SEQUENCE 476 AA; 52170 MW; 9B36D1BA6109B46E CRC64;  
 Q9LK41 Length: 476 October 13, 2004 13:38 Type: P Check: 2170  
 Found using 'claim36' (zara371.key)

386 WVCVAVDGADEALGQALNPFACGRSNATCALAPGEGYAPVTVTWHSYATSSYWAQFR  
 436 444

446 NOSOCYFNGLARETTTPGNERCKEPPSVTL

-----  
 1 match found in sequence:  
 g9sfw1; Putative beta-1,3-glucanase.  
 (from "claim36spt.pep")  
 TOIG of: g9sfw1 check: 9732 from: 1 to: 440

ID Q9SFW1 PRELIMINARY; PRT; 440 AA.  
 AC Q9SFW1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Putative beta-1,3-glucanase.  
 GN T1B9.1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,  
 RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome III BAC T1B9 genomic sequence."  
 RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AC012395; AAF20214.1; -  
 DR HSSP; P12257; IAO0.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000490; Glyco\_hydro\_17.  
 DR Pfam; PF00332; Glyco\_hydro\_17; 1.  
 DR PROSITE; PS00587; GLYCOSYL\_HYDROL\_F17; 1.  
 SQ SEQUENCE 440 AA; 48538 MW; FC8B6A3B384BBD93 CRC64;  
 Q9SFW1 Length: 440 October 13, 2004 13:38 Type: P Check: 9732  
 Found using 'claim36' (zara371.key)

350 KTEYKESLPAPENNNDLYKGIKWCVGNNTCDPIRGGPOCKEDLTVLHASYSYWAQFR  
 400 408

410 KIGTCSFNGLATQTIKDPYGRCEPPSVTL

-----  
 1 match found in sequence:  
 g9sfw1; Putative glucan endo-1,3-beta-glucosidase (putative beta-1,3-glucanas  
 (from "claim36spt.pep")  
 TOIG of: g9sfw1 check: 8766 from: 1 to: 460

ID Q9SFW1 PRELIMINARY; PRT; 460 AA.  
 AC Q9SFW1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Putative glucan endo-1,3-beta-glucosidase (putative beta-1,3-glucanase  
 precursor) (putative glycosyl hydrolase).  
 GN F2103.3 OR AT3G07320/T1B9.1 OR AT3G07320.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,  
 RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome III BAC F2103 genomic sequence."  
 RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.

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RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Arabidopsis thaliana full-length cDNA.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Omodesa C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shimizu P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Eckert J.R.,
RA Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC009853; AF02143.1; -
DR EMBL: AK18068; BC04269.1; -
DR EMBL: BT005678; AA064098.1; -
DR HSSP: P12257; 1A00.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR000490; Glyco_hydro_17; 1.
DR Pfam: PF00332; Glyco_hydro_17; 1.
DR PROSITE: PS00587; GLYCOSYL_HYDROL_F17; 1.
KW Hydrolyase.
SQ SEQUENCE 460 AA; 50603 MW; D2061EAA09C0F85F CRC64;
Q9SR74 Length: 460 October 13, 2004 13:38 Type: P Check: 8766 ..
Found using 'claim36' (zara371.key)
...
370 IWCVAKGANWTQLGDLALSYACSGGANTCPDIQRGPGQKDLTVLHASYAFSSYMAQFR
-----|
420 428
430 KIGGTCSFNGLATQTIKDPSYGRCEPFSVTL
-----|
1 match found in sequence:
q9vdv4; CG16718 protein.
(from "claim36spt.pep")
TOIG of: q9vdv4 check: 1097 from: 1 to: 1075
ID Q9VDV4 PRELIMINARY; PRT; 1075 AA.
AC Q9VDV4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG16718 protein.
GN CG16718.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey J.-G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.A., Bouck J., Brokerlein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murty D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Teetor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003727; AAP5685.1; -
DR FlyBase; FBgn0038721; CG16718.
DR InterPro: IPR007632; DUF590.
DR Pfam; PF04547; DUF590; 1.
SQ SEQUENCE 1075 AA; 123934 MW; 729765FBD8339C70 CRC64;
Q9VDV4 Length: 1075 October 13, 2004 13:38 Type: P Check: 1097 ..
Found using 'claim36' (zara371.key)
...
451 VPKYDIOGSGNTNITMCPICDWCNPFMDIKETCNVAKVTYLLIDNPSTVFPVFPSPATLTF
-----|
501 509
511 LELMKRYSAEITRMDLTFGPDVHEHPRPOLYRLERHIPPTRVDVYNTNI
-----|

```

```

-- Search Statistics --
Times: CPU Total Elapsed
00:00:00.00 00:00:00.00
Number of sequences searched: 11
Number of sequence hits: 11
Number of separate matches: 11
Number of sequence hits saved: 0

```

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0 | 0 Intelligenetics  
> 0 <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "claim36\_pir" --

Selected search type is key against sequence data banks or files.  
Selected scope is Sequence.

Selected sequence key from "zara371.key":

claim36 (AA) ID claim36 AA preliminary pattern

followed by

```
1 r or n or a or t or v
2 f
2 m or l or t or r or a or s
2 r or h or e or c or s or d
2 h or f or y
2 w
2 e or t or a or f or s
2 g or q or t or a or d
2 f or q or l
```

Selected files:

File : claim36pir.pep

-- Output Parameters --

Format Options:

Nucleic acid code matching	Exact	Indirect file	No
Find non-matching hits only	No	Sequence or key file	No
Report key used	Yes	List of hits	Yes
Note position of hit	Yes	Hit display	Yes
Display full annotations	Yes	Name and annotations	Yes
Sequence context	50		

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

s31612 ; TOIG of: s31612 check: 219 from: 1 to: 139

(from "claim36pir.pep")

TOIG of: s31612 check: 219 from: 1 to: 139

F1:S31612 - beta-1,3-glucanase homolog (clone A20) - rape (fragment)

C:Species: Brassica napus (rape)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Nov-2000

C:Accession: S31612

R:Hard, D.; Worral, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.

submitted to the EMBL Data Library, December 1992

A:Description: The anther-specific protein encoded by the Brassica napus and

Arabidopsis thaliana A6 gene exhibits homology to beta-1,3-glucanases.

A:Reference number: S31612

A:Accession: S31612

A:Molecule type: mRNA

A:Residues: 1-139 <HIR>

A:Cross-references: EMBL:X69889; NID:G17733; PID:G17734

A:Experimental source: clone A20

C:Superfamily: beta-1,3-glucanase

S31612 Length: 139 October 13, 2004 13:40 Type: P Check: 219 ..

Found using 'claim36' (zara371.key)

49 VMCVAVGANETELGALDFACGRSNATCAALAPGRECVAPVETWHASAFSSYNAQFR 99 107

109 NQSSQCFNGLARETTTTPGNEQCKFPSTVL

1 match found in sequence:

s74688 ; TOIG of: s74688 check: 9387 from: 1 to: 391

(from "claim36pir.pep")

TOIG of: s74688 check: 9387 from: 1 to: 391

P1:S74688 - hypothetical protein s111200 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999

C:Accession: S74688

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;

Miyajima, N.; Hirose, M.; Sugitani, M.; Sasamoto, S.; Kimura, T.; Hosouchi,

T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.;

Takeuchi, C.; Wada, T.; Matanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and

assignment of potential protein-coding regions.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74688

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-391 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:G1651897; PIDN:BA16839.1;

PID:dl017572; PID:G1651913

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June

1996

S74688 Length: 391 October 13, 2004 13:40 Type: P Check: 9387 ..

Found using 'claim36' (zara371.key)

296 FWDPAFAFSLWLGSSILNNGLIPLELLEILOGNQTGVGIGLFGCVGLAGDVFTRRYSTQS 346 354

356 SQMHGGLGLMLVMSITLCCARYWQGFRRPKKGAGD

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of sequences searched: 2

Number of sequence hits: 2

Number of separate matches: 2

Number of sequence hits saved: 0

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! FINDPATTERNS on Swiss-Prot: \* allowing 0 mismatches

! 1 (R,N,A,T,V)F(M,I,T,R,A,S)(R,H,E,C,S,D)(H,F,Y)W(E,T,A,F,S)(G,Q,T,A,D)(F,Q,L)

Databases searched:

SWISS-PROT, Release 42.7, Released on 15Dec2003, Formatted on 15Dec2003

Total finds:

0

Total length:

52,070,155

Total sequences:

141,681

CPU time:

03:00.75

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> O <  
O | O IntelliGenetics  
> O <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "claim36\_age" --

Selected search type is key against sequence data banks or files.  
Selected scope is Sequence.

Selected sequence key from "zara371.key":

claim36 (AA) ID claim36 AA preliminary pattern

followed by

```
1 r or n or a or t or v
2 f
2 m or i or t or r or a or s
2 r or h or e or c or s or d
2 h or f or y
2 w
2 e or t or a or f or s
2 g or q or t or a or d
2 f or q or l
```

Selected files:

File : claim36ags.pep

-- Output Parameters --

Format Options:

File Options:	Exact	Indirect file	No
Nucleic acid code matching	No	Sequence or key file	No
Find non-matching hits only	Yes	List of hits	Yes
Report key used	Yes	Hit display	Yes
Note position of hit	Yes	Name and annotations	Yes
Display full annotations	Yes		Yes
Sequence context	50		

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

aab17079 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:135.

(from "claim36ags.pep")

TOIG of: aab17079 check: 5978 from: 1 to: 12

ID AAB17079 standard; peptide; 12 AA.

XX AAB17079;

DT 31-OCT-2000 (first entry)

XX Mdm/hdm antagonist peptide sequence SEQ ID NO:135.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
XX cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
XX vascular endothelial growth factor; matrix metalloproteinase; asthma;  
XX thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

PN 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US025044.  
XX  
PR 23-OCT-1998; 98US-0105371P.  
PR 22-OCT-1999; 99US-00428082.  
XX  
XX (AMGE-) AMGEN INC.  
PI Feige U, Liu C, Cheetham J, Boone TC;  
XX WPI, 2000-350702/30.  
XX  
XX Novel composition of matter comprising an Fc domain and pharmacologically  
PT active peptides, useful for treating cancer and autoimmune diseases.  
XX  
PS Claim 39; Page 241; 608pp; English.

XX The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-  
CC (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,  
CC P3, and P4 = are each independently sequences of pharmacologically active  
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1  
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,  
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host  
CC cells from the present invention can be used for producing pharmaceutical  
CC compositions. The compositions are useful for treating cancer, asthma,  
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
CC a Fab domain) can provide a longer half-life or incorporate functions  
CC such as Fc receptor binding, protein A binding, complement fixation, and  
CC possibly placental transfer. AA6943 to AA6956 and AAB16955 to  
CC AAB18003 represent nucleotide and amino acid sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 12 AA;

AA17079 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..  
Found using 'claim36' (zara371.key)

1 |-----|  
MPRFMDYWGELN  
3 11

1 match found in sequence:  
aab17080 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:136.  
(from "claim36ags.pep")  
TOIG of: aab17080 check: 6151 from: 1 to: 12

ID AAB17080 standard; peptide; 12 AA.

XX AAB17080;

DT 31-OCT-2000 (first entry)

XX Mdm/hdm antagonist peptide sequence SEQ ID NO:136.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
XX cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
XX vascular endothelial growth factor; matrix metalloproteinase; asthma;  
XX thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

PN 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US025044.

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XX 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX
XX Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
XX
XX Claim 39; Page 242; 608pp; English.
XX
XX The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
XX independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
XX (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
XX P3, and P4 = are each independently sequences of pharmacologically active
XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX of a and b is 1. The composition can have cytostatic, antiaesthetic,
XX thrombolytic and immunosuppressive activities. DNAs, vectors and host
XX cells from the present invention can be used for producing pharmaceutical
XX compositions. The compositions are useful for treating cancer, asthma,
XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
XX a Fab domain) can provide a longer half-life or incorporate functions
XX such as Fc receptor binding, protein A binding, complement fixation, and
XX possibly placental transfer. AA69443 to AA69526 and AAB16955 to
XX AAB18003 represent nucleotide and amino acid sequences used in the
XX exemplification of the present invention
XX
XX SQ Sequence 12 AA:
XX
AAB17080 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..
Found using 'claim36' (zara371.key)
1
1 -----|
  VONFIDYWTQOF
  3
  11
-----|
1 match found in sequence:
aab17081; Mdm/hdm antagonist peptide sequence SEQ ID NO:137.
(from "claim36ags.pep")
TOIG of: aab17081 check: 5993 from: 1 to: 12
ID AAB17081 standard; peptide, 12 AA.
XX
XX AAB17081;
XX
AC AAB17082;
XX
DT 31-OCT-2000 (first entry)
XX
DE Mdm/hdm antagonist peptide sequence SEQ ID NO:137.
XX
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX vascular endothelial growth factor; matrix metalloproteinase; asthma;
XX thrombosis; pharmaceutical.
XX
XX Synthetic.
XX
XX WO200024782-A2.
XX
XX 04-MAY-2000.
XX
XX 25-OCT-1999; 99WO-US025044.
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XX

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PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX
XX Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
XX
XX Claim 39; Page 242; 608pp; English.
XX
XX The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
XX independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
XX (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
XX P3, and P4 = are each independently sequences of pharmacologically active
XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX of a and b is 1. The composition can have cytostatic, antiaesthetic,
XX thrombolytic and immunosuppressive activities. DNAs, vectors and host
XX cells from the present invention can be used for producing pharmaceutical
XX compositions. The compositions are useful for treating cancer, asthma,
XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
XX a Fab domain) can provide a longer half-life or incorporate functions
XX such as Fc receptor binding, protein A binding, complement fixation, and
XX possibly placental transfer. AA69443 to AA69526 and AAB16955 to
XX AAB18003 represent nucleotide and amino acid sequences used in the
XX exemplification of the present invention
XX
XX SQ Sequence 12 AA:
XX
AAB17081 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..
Found using 'claim36' (zara371.key)
1
1 -----|
  TGPAPFTHWATF
  4
  12
-----|
1 match found in sequence:
aab17082; Mdm/hdm antagonist peptide sequence SEQ ID NO:138.
(from "claim36ags.pep")
TOIG of: aab17082 check: 9093 from: 1 to: 15
ID AAB17082 standard; peptide, 15 AA.
XX
XX AAB17082;
XX
AC AAB17082;
XX
DT 31-OCT-2000 (first entry)
XX
DE Mdm/hdm antagonist peptide sequence SEQ ID NO:138.
XX
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX vascular endothelial growth factor; matrix metalloproteinase; asthma;
XX thrombosis; pharmaceutical.
XX
XX Synthetic.
XX
XX WO200024782-A2.
XX
XX 04-MAY-2000.
XX
XX 25-OCT-1999; 99WO-US025044.
XX
XX 23-OCT-1998; 98US-0105371P.
XX
XX

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PR 22-OCT-1999; 99US-00428082.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Feige U, Liu C, Cheetham J, Boone TC;  
XX WPI; 2000-350702/30.  
DR  
XX  
PT Novel composition of matter comprising an Fc domain and pharmacologically  
PT active peptides, useful for treating cancer and autoimmune diseases.  
XX  
XX Claim 39; Page 242; 608pp; English.  
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XX The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-  
CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,  
CC P3, and P4 = are each independently sequences of pharmacologically active  
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1  
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,  
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host  
CC cells from the present invention can be used for producing pharmaceutical  
CC compositions. The compositions are useful for treating cancer, asthma,  
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
CC a Fab domain) can provide a longer half-life or incorporate functions  
CC such as Fc receptor binding, protein A binding, complement fixation, and  
CC possibly placental transfer. AA69443 to AA69526 and AAB1955 to  
CC AAB18003 represent nucleotide and amino acid sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 15 AA:  
SQ  
AAB17082 Length: 15 October 13, 2004 13:39 Type: P Check: 9093 ..  
Found using 'claim36' (zara371.key)  
1  
1 -----  
6 IDRAPTRDHWFPALV  
14  
-----  
1 match found in sequence:  
aab17083; Mdm/hdm antagonist peptide sequence SEQ ID NO:139.  
(from "claim36ags.pep")  
TOIG of: aab17083 Check: 9428 from: 1 to: 15  
ID AAB17083 standard; peptide; 15 AA.  
XX  
XX AAB17083;  
AC  
XX  
DT 31-OCT-2000 (first entry)  
XX  
XX Mdm/hdm antagonist peptide sequence SEQ ID NO:139.  
DE  
XX  
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;  
KW thrombosis; pharmaceutical.  
XX  
XX Synthetic.  
OS  
XX  
XX WO200024782-A2.  
PN  
XX  
XX 04-MAY-2000.  
PD  
XX  
XX 25-OCT-1999; 99WO-US025044.  
PF  
XX  
XX 23-OCT-1998; 98US-0105371P.  
PR  
XX  
XX 22-OCT-1999; 99US-00428082.

XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Feige U, Liu C, Cheetham J, Boone TC;  
XX WPI; 2000-350702/30.  
DR  
XX  
PT Novel composition of matter comprising an Fc domain and pharmacologically  
PT active peptides, useful for treating cancer and autoimmune diseases.  
XX  
XX Claim 39; Page 243; 608pp; English.  
XX  
XX The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-  
CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,  
CC P3, and P4 = are each independently sequences of pharmacologically active  
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1  
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,  
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host  
CC cells from the present invention can be used for producing pharmaceutical  
CC compositions. The compositions are useful for treating cancer, asthma,  
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
CC a Fab domain) can provide a longer half-life or incorporate functions  
CC such as Fc receptor binding, protein A binding, complement fixation, and  
CC possibly placental transfer. AA69443 to AA69526 and AAB1955 to  
CC AAB18003 represent nucleotide and amino acid sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 15 AA:  
SQ  
AAB17083 Length: 15 October 13, 2004 13:39 Type: P Check: 9428 ..  
Found using 'claim36' (zara371.key)  
1  
1 -----  
6 PRPALVADYWTETLY  
14  
-----  
1 match found in sequence:  
aab17084; Mdm/hdm antagonist peptide sequence SEQ ID NO:140.  
(from "claim36ags.pep")  
TOIG of: aab17084 Check: 8833 from: 1 to: 15  
ID AAB17084 standard; peptide; 15 AA.  
XX  
XX AAB17084;  
AC  
XX  
DT 31-OCT-2000 (first entry)  
XX  
XX Mdm/hdm antagonist peptide sequence SEQ ID NO:140.  
DE  
XX  
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;  
KW thrombosis; pharmaceutical.  
XX  
XX Synthetic.  
OS  
XX  
XX WO200024782-A2.  
PN  
XX  
XX 04-MAY-2000.  
PD  
XX  
XX 25-OCT-1999; 99WO-US025044.  
PF  
XX  
XX 23-OCT-1998; 98US-0105371P.  
PR  
XX  
XX 22-OCT-1999; 99US-00428082.





PR 19-JUL-1999;	99US-0144333P.	PR 13-OCT-1999;	99US-0159295P.
PR 19-JUL-1999;	99US-0144334P.	PR 14-OCT-1999;	99US-0159329P.
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PR 20-JUL-1999;	99US-0144352P.	PR 14-OCT-1999;	99US-0159331P.
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PR 21-JUL-1999;	99US-0144814P.	PR 18-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145085P.	PR 21-OCT-1999;	99US-0160768P.
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PR 23-JUL-1999;	99US-0145182P.	PR 21-OCT-1999;	99US-0160815P.
PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160980P.
PR 23-JUL-1999;	99US-0145218P.	PR 22-OCT-1999;	99US-0160981P.
PR 23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;	99US-0160989P.
PR 26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;	99US-0161040P.
PR 27-JUL-1999;	99US-0145913P.	PR 25-OCT-1999;	99US-0161405P.
PR 27-JUL-1999;	99US-0145919P.	PR 25-OCT-1999;	99US-0161406P.
PR 28-JUL-1999;	99US-0145951P.	PR 26-OCT-1999;	99US-0161359P.
PR 02-AUG-1999;	99US-0146386P.	PR 26-OCT-1999;	99US-0161360P.
PR 02-AUG-1999;	99US-0146388P.	PR 26-OCT-1999;	99US-0161361P.
PR 02-AUG-1999;	99US-0146389P.	PR 28-OCT-1999;	99US-0161920P.
PR 03-AUG-1999;	99US-0147038P.	PR 28-OCT-1999;	99US-0161922P.
PR 04-AUG-1999;	99US-0147204P.	PR 29-OCT-1999;	99US-0162142P.
PR 04-AUG-1999;	99US-0147302P.	PR 29-OCT-1999;	99US-0162143P.
PR 05-AUG-1999;	99US-0147192P.	PR 29-OCT-1999;	99US-0162228P.
PR 05-AUG-1999;	99US-0147260P.	PR 01-NOV-1999;	99US-0162891P.
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PR 10-AUG-1999;	99US-0148317P.	PR 02-NOV-1999;	99US-0163093P.
PR 11-AUG-1999;	99US-0148319P.	PR 03-NOV-1999;	99US-0163248P.
PR 12-AUG-1999;	99US-0148341P.	PR 03-NOV-1999;	99US-0163249P.
PR 13-AUG-1999;	99US-0148565P.	PR 04-NOV-1999;	99US-0163281P.
PR 13-AUG-1999;	99US-0148684P.	PR 04-NOV-1999;	99US-0163380P.
PR 16-AUG-1999;	99US-0149368P.	PR 04-NOV-1999;	99US-0163381P.
PR 17-AUG-1999;	99US-0149375P.	PR 08-NOV-1999;	99US-0164146P.
PR 18-AUG-1999;	99US-0149426P.	PR 08-NOV-1999;	99US-0164150P.
PR 20-AUG-1999;	99US-0149722P.	PR 09-NOV-1999;	99US-0164151P.
PR 20-AUG-1999;	99US-0149723P.	PR 09-NOV-1999;	99US-0164259P.
PR 20-AUG-1999;	99US-0149929P.	PR 09-NOV-1999;	99US-0164260P.
PR 23-AUG-1999;	99US-0149930P.	PR 10-NOV-1999;	99US-0164317P.
PR 25-AUG-1999;	99US-0150566P.	PR 10-NOV-1999;	99US-0164318P.
PR 26-AUG-1999;	99US-0150884P.	PR 10-NOV-1999;	99US-0164319P.
PR 27-AUG-1999;	99US-0151065P.	PR 10-NOV-1999;	99US-0164321P.
PR 27-AUG-1999;	99US-0151066P.	PR 10-NOV-1999;	99US-0164544P.
PR 30-AUG-1999;	99US-0151303P.	PR 10-NOV-1999;	99US-0164545P.
PR 31-AUG-1999;	99US-015138P.	PR 12-NOV-1999;	99US-0164548P.
PR 01-SEP-1999;	99US-0151930P.	PR 12-NOV-1999;	99US-0164670P.
PR 07-SEP-1999;	99US-0152363P.	PR 12-NOV-1999;	99US-0164871P.
PR 10-SEP-1999;	99US-0153070P.	PR 12-NOV-1999;	99US-0164959P.
PR 13-SEP-1999;	99US-0153758P.	PR 12-NOV-1999;	99US-0164960P.
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PR 20-SEP-1999;	99US-0154779P.	PR 15-NOV-1999;	99US-0164927P.
PR 22-SEP-1999;	99US-0155139P.	PR 15-NOV-1999;	99US-0164929P.
PR 23-SEP-1999;	99US-0155486P.	PR 16-NOV-1999;	99US-0165661P.
PR 24-SEP-1999;	99US-0155659P.	PR 16-NOV-1999;	99US-0165669P.
PR 28-SEP-1999;	99US-0156458P.	PR 16-NOV-1999;	99US-0165671P.
PR 29-SEP-1999;	99US-0156596P.	PR 17-NOV-1999;	99US-0165911P.
PR 04-OCT-1999;	99US-0157117P.	PR 17-NOV-1999;	99US-0165918P.
PR 05-OCT-1999;	99US-0157753P.	PR 18-NOV-1999;	99US-0165919P.
PR 06-OCT-1999;	99US-0157865P.	PR 18-NOV-1999;	99US-0166157P.
PR 07-OCT-1999;	99US-0158029P.	PR 18-NOV-1999;	99US-0166158P.
PR 08-OCT-1999;	99US-0158232P.	PR 18-NOV-1999;	99US-0166173P.
PR 12-OCT-1999;	99US-0158369P.	PR 19-NOV-1999;	99US-0166411P.
PR 13-OCT-1999;	99US-0159293P.	PR 19-NOV-1999;	99US-0166412P.
PR 13-OCT-1999;	99US-0159294P.	PR 19-NOV-1999;	99US-0166419P.

[illegible]

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CC thaliana. its coding sequence was isolated by carrying out RT-PCR on all
CC of the mRNA obtained from the plant, and creating a cDNA library which
CC could then be sequenced, allowing the putative protein sequence(s) to be
CC obtained. This sequence may be useful for protein identification and for
CC aiding in the elucidation of signal transduction and metabolic pathways.
CC Its coding sequence has a use in the control of gene expression as a
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC the behaviour of a gene within the chromosome, as a tool for use in
CC genetic mapping, including a use in hybridisation assays, for recognition
CC or isolation of similar DNA fragments, or for the identification of a
CC particular organism
XX
SQ Sequence 493 AA;
AG07078 Length: 493 October 13, 2004 13:39 Type: P Check: 9327 ..
Found using 'claim36' (zara371.key)
...
403 IMCVAKGANWTLGDPALSYACSGNNTCDFIORGGPCQKPDLTVLHASYAFSSWAOFR
|-----|
453 461
463 KIGCTCSFNGLAITQTIKDPSEYGRCPSPVTL
-----
1 match found in sequence:
aag07079; Arabidopsis thaliana protein fragment SEQ ID NO: 4093.
(from "claim36gs.pep")
TOIG of: aag07079 check: 8289 from: 1 to: 460
ID AAG07079 standard; protein; 460 AA.
XX
XX AAG07079;
XX
XX DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4093.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX
XX 06-SEP-2000.
XX
XX PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
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 XX Zheng L, Dumas J;  
 PI WPI, 2000-507395/46.  
 DR N-PSDB; AAC3724.  
 DR XX  
 PT New sequence determined DNA fragments (SDPs) from different plant  
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 PT sequences.  
 PT  
 XX Claim 19; SEQ ID NO 4093; 344pp + Sequence listing; English.  
 XX  
 XX The present sequence is a putative protein fragment from Arabidopsis  
 CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
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 CC could then be sequenced, allowing the putative protein sequence(s) to be  
 CC obtained. This sequence may be useful for protein identification and for  
 CC aiding in the elucidation of signal transduction and metabolic pathways.  
 CC Its coding sequence has a use in the control of gene expression as a  
 CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
 CC the behaviour of a gene within the chromosome, as a tool for use in  
 CC genetic mapping, including a use in hybridisation assays, for recognition  
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XX 17-OCT-2000 (first entry)

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hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

XX Arabidopsis thaliana.

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XX (CERE-) CERES INC.  
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L, Dumas J;  
XX WPI: 2000-507395/46.  
DR N-PSDB; AAC33724.  
XX  
XX New sequence determined DNA fragments (SDPs) from different plant  
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,  
PT protein coding sequences, untranslated regions, or as 3' termination  
PT sequences.  
XX  
PS Claim 19; SEQ ID NO 4094; 344bp + Sequence listing; English.  
XX  
XX The present sequence is a putative protein fragment from Arabidopsis  
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
CC of the mRNA obtained from the plant, and creating a cDNA library which  
CC could then be sequenced, allowing the putative protein sequence(s) to be  
CC obtained. This sequence may be useful for protein identification and for  
CC aiding in the elucidation of signal transduction and metabolic pathways.  
CC Its coding sequence has a use in the control of gene expression as a  
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
CC the behaviour of a gene within the chromosome, as a tool for use in  
CC genetic mapping, including a use in hybridisation assays, for recognition  
CC or isolation of similar DNA fragments, or for the identification of a  
CC particular organism  
XX  
SQ Sequence 384 AA;  
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DT 17-OCT-2000 (first entry)  
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 XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
 PI Zheng L, Dumas J;  
 XX  
 XX WPI; 2000-507395/46.  
 DR N-PSDB; AAC34196.  
 DR  
 PT New sequence determined DNA fragments (SDPs) from different plant  
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,  
 PT protein coding sequences, untranslated regions, or as 3' termination  
 PT sequences.  
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 XX Claim 19; SEQ ID NO 5798; 344pp + Sequence listing; English.  
 XX  
 CC The present sequence is a putative protein fragment from Arabidopsis  
 CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
 CC of the mRNA obtained from the plant, and creating a cDNA library which  
 CC could then be sequenced, allowing the putative protein sequence(s) to be  
 CC obtained. This sequence may be useful for protein identification and for  
 CC aiding in the elucidation of signal transduction and metabolic pathways.  
 CC Its coding sequence has a use in the control of gene expression as a  
 CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
 CC the behaviour of a gene within the chromosome, as a tool for use in  
 CC genetic mapping, including a use in hybridisation assays, for recognition  
 CC or isolation of similar DNA fragments, or for the identification of a  
 CC particular organism  
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 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
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XX (CERE-) CERES INC.  
PA Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L, Dumas J;  
XX WPI, 2000-507395/46.  
DR N-PSDB; AAC34196.  
XX  
PT New sequence determined DNA fragments (SDFs) from different plant  
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,  
PT protein coding sequences, untranslated regions, or as 3' termination  
PT sequences.  
XX  
PS Claim 19; SEQ ID NO 5799; 344pp + Sequence listing; English.  
XX  
CC The present sequence is a putative protein fragment from Arabidopsis  
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
CC of the mRNA obtained from the plant, and creating a cDNA library which  
CC could then be sequenced, allowing the putative protein sequence(s) to be  
CC obtained. This sequence may be useful for protein identification and for  
CC aiding in the elucidation of signal transduction and metabolic pathways.  
CC Its coding sequence has a use in the control of gene expression as a  
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
CC the behaviour of a gene within the chromosome, as a tool for use in  
CC genetic mapping, including a use in hybridisation assays, for recognition  
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PA (CERE-) CERES INC.  
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L, Dumas J;  
XX WPI; 2000-507395/46.  
XX N-PSDB; AAC34196.  
PT New sequence determined DNA fragments (SDFs) from different plant  
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,  
PT protein coding sequences, untranslated regions, or as 3' termination  
XX sequences.

PS Claim 19; SEQ ID NO 5800; 344bp + Sequence Listing; English.  
XX  
XX The present sequence is a putative protein fragment from Arabidopsis  
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
CC of the mRNA obtained from the plant, and creating a cDNA library which  
CC could then be sequenced, allowing the putative protein sequence(s) to be  
CC obtained. This sequence may be useful for protein identification and for  
CC aiding in the elucidation of signal transduction and metabolic pathways.  
CC Its coding sequence has a use in the control of gene expression as a  
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
CC the behaviour of a gene within the chromosome, as a tool for use in  
CC genetic mapping, including a use in hybridisation assays for recognition  
CC or isolation of similar DNA fragments, or for the identification of a  
CC particular organism  
XX  
SQ Sequence 388 AA;  
AA08314 Length: 388 October 13, 2004 13:39 Type: P Check: 1549 ..  
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348 356  
358 NOSSQCYFNGLARETTTNPGERCKRFPSTVL  
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1 match found in sequence:  
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AC  
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DT 18-OCT-2000 (first entry)  
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 48177.  
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XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX EP1033405-A2.  
PN  
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XX  
PF 25-FEB-2000; 2000EP-00301439.  
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PA	(CERE-) CERES INC.	
XX		
PI	Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;	
PI	Zheng L, Dumas J;	
XX		
DR	WPI; 2000-507395/46.	
DR	N-PSDB; AAC45900.	
XX		
PT	New sequence determined DNA fragments (SDFs) from different plant	
PT	species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,	
PT	protein coding sequences, untranslated regions, or as 3' termination	
PT	sequences.	
XX		
PS	Claim 19; SEQ ID NO 48177; 344bp + Sequence Listing; English.	
XX		
CC	The present sequence is a putative protein fragment from Arabidopsis	
CC	thaliana. Its coding sequence was isolated by carrying out RT-PCR on all	
CC	of the mRNA obtained from the plant, and creating a cDNA library which	
CC	could then be sequenced, allowing the putative protein sequence(s) to be	
CC	obtained. This sequence may be useful for protein identification and for	
CC	aiding in the elucidation of signal transduction and metabolic pathways.	
CC	Its coding sequence has a use in the control of gene expression as a	
CC	promoter, coding sequence, 3'UTR or transmembrane sequence, for controlling	
CC	the behaviour of a gene within the chromosome, as a tool for use in	
CC	genetic mapping, including a use in hybridisation assays, for recognition	
CC	or isolation of similar DNA fragments, or for the identification of a	
CC	particular organism	



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463      KIGGTCSFNGLATQTIKDPGYGRCEPSSVTL

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(from "claim36ags.dep")
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DT      18-OCT-2000 (first entry)
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KW      hybridization assay; genetic mapping; gene expression control; promoter;
KW      termination sequence.
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XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L, Dumas J;  
XX  
XX MPI: 2000-507395/46.  
DR N-PSDB; AAC45300.  
XX  
XX New sequence determined DNA fragments (SDFs) from different plant  
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,  
PT protein coding sequences, untranslated regions, or as 3' termination  
PT sequences.  
XX  
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XX  
XX The present sequence is a putative protein fragment from Arabidopsis  
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
CC of the mRNA obtained from the plant, and creating a cDNA library which  
CC could then be sequenced, allowing the putative protein sequence(s) to be  
CC obtained. This sequence may be useful for protein identification and for  
CC aiding in the elucidation of signal transduction and metabolic pathways.  
CC Its coding sequence has a use in the control of gene expression as a  
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
CC the behaviour of a gene within the chromosome, as a tool for use in  
CC genetic mapping, including a use in hybridisation assays, for recognition  
CC or isolation of similar DNA fragments, or for the identification of a  
CC particular organism  
XX  
XX  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
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XX
XX (CERE-) CERES INC.
XX
XX PA
XX PI Alexandrov N, Brover V, Chen X, Sudramanian G, Troukhan ME;
XX PI Zheng L, Dumas J;
XX DR MPI; 2000-507395/46.
XX DR N-PSDB; AAC45900.
XX
XX PT New sequence determined DNA fragments (SDPs) from different plant
XX PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
XX PT protein coding sequences, untranslated regions, or as 3' termination
XX PT sequences.
XX
XX Claim 19; SEQ ID NO 48179; 344pp + Sequence Listing; English.
XX
XX CC The present sequence is a putative protein fragment from Arabidopsis
XX CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
XX CC of the mRNA obtained from the plant, and creating a cDNA library which
XX CC could then be sequenced, allowing the putative protein sequence(s) to be
XX CC obtained. This sequence may be useful for protein identification and for
XX CC aiding in the elucidation of signal transduction and metabolic pathways.
XX CC Its coding sequence has a use in the control of gene expression as a
XX CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
XX CC the behaviour of a gene within the chromosome, as a tool for use in
XX CC genetic mapping, including a use in hybridisation assays, for recognition
XX CC or isolation of similar DNA fragments, or for the identification of a
XX CC particular organism
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KW Protein identification; signal transduction pathway; metabolic pathway;  
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XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L, Dumas J;  
XX WPI; 2000-507395/46.  
DR N-PSDB; AAC50943.  
XX  
XX  
XX New sequence determined DNA fragments (SDPs) from different plant  
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,  
PT protein coding sequences, untranslated regions, or as 3' termination  
PT sequences.  
XX  
XX  
XX Claim 19; SEQ ID NO 66706; 344pp + Sequence Listing; English.  
XX  
XX The present sequence is a putative protein fragment from Arabidopsis  
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
CC of the mRNA obtained from the plant, and creating a cDNA library which  
CC could then be sequenced, allowing the putative protein sequence(s) to be  
CC obtained. This sequence may be useful for protein identification and for  
CC aiding in the elucidation of signal transduction and metabolic pathways.  
CC Its coding sequence has a use in the control of gene expression as a  
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
CC the behaviour of a gene within the chromosome, as a tool for use in  
CC genetic mapping, including a use in hybridisation assays, for recognition  
CC or isolation of similar DNA fragments, or for the identification of a  
CC particular organism  
XX  
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 PA (CERE-) CERES INC.  
 PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
 PI Zheng L, Dumas U;  
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 XX WPI; 2000-507395/46.  
 DR N-PSDB; AAC50943.  
 XX  
 XX  
 PT New sequence determined DNA fragments (SDPs) from different plant  
 species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,

PT protein coding sequences, untranslated regions, or as 3' termination  
 PT sequences.  
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 XX  
 PS Claim 19; SEQ ID NO 66707; 344pp + Sequence Listing; English.  
 XX  
 CC The present sequence is a putative protein fragment from Arabidopsis  
 CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
 CC of the mRNA obtained from the plant, and creating a cDNA library which  
 CC could then be sequenced, allowing the putative protein sequence(s) to be  
 CC obtained. This sequence may be useful for protein identification and for  
 CC aiding in the elucidation of signal transduction and metabolic pathways.  
 CC Its coding sequence has a use in the control of gene expression as a  
 CC promoter, coding sequence, 3' UTR or termination sequence, for controlling  
 CC the behaviour of a gene within the chromosome, as a tool for use in  
 CC genetic mapping, including a use in hybridisation assays, for recognition  
 CC or isolation of similar DNA fragments, or for the identification of a  
 CC particular organism  
 XX  
 SQ Sequence 476 AA;  
 AAG52474 Length: 476 October 13, 2004 13:39 Type: P Check: 2170  
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 AC AAG52475;  
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 DT 18-OCT-2000 (first entry)  
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 DE Arabidopsis thaliana protein fragment SEQ ID NO: 66708.  
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 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
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 XX  
 XX Claim 19; SEQ ID NO 66708; 344pp + Sequence Listing; English.  
 CC The present sequence is a putative protein fragment from Arabidopsis  
 CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all  
 CC of the mRNA obtained from the plant, and creating a cDNA library which  
 CC could then be sequenced, allowing the putative protein sequence(s) to be  
 CC obtained. This sequence may be useful for protein identification and for  
 CC aiding in the elucidation of signal transduction and metabolic pathways.  
 CC Its coding sequence has a use in the control of gene expression as a  
 CC promoter, coding sequence, 3'UTR or termination sequence, for controlling  
 CC the behaviour of a gene within the chromosome, as a tool for use in

CC genetic mapping, including a use in hybridisation assays, for recognition  
 CC or isolation of similar DNA fragments, or for the identification of a  
 CC particular organism  
 XX  
 SQ Sequence 388 AA;  
 AAG52475 Length: 388 October 13, 2004 13:39 Type: P Check: 1903 ..  
 Found using 'claim36' (zara371.key)

298 VMCVAVGADAEALGALNFACGRSNATCAALAPGECYAPVTWTWIASYAFSSYMAQFR  
 348 356

358 NOSSQCYFNGLAARETTTNGNERCKEPPSVTL

-----  
 1 match found in sequence:  
 aaw37170 : Human oncogenic protein MDM2 binding peptide 1.  
 (from "claim36ags.pep")  
 TOIG of: aaw37170 Check: 5978 From: 1 to: 12

ID AAW37170 standard; peptide; 12 AA.  
 XX  
 AC AAW37170;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE Human oncogenic protein MDM2 binding peptide 1.  
 XX  
 KM MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 XX tumour; diagnosis; binding; viral infection.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9801467-A2.  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 04-JUL-1997; 97WO-EP003549.  
 XX  
 PR 05-JUL-1996; 96GB-00014197.  
 XX  
 PR 07-APR-1997; 97GB-00007041.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 XX  
 DR WPI; 1998-100996/09.  
 XX  
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.  
 XX  
 PS Claim 5; Page 41; 45pp; English.  
 XX  
 CC This peptide is capable of binding to an oncogenic protein MDM2  
 CC (especially human MDM2). The MDM2 binding peptides can specifically  
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can  
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type  
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify  
 CC molecules that bind to MDM2 and to identify and design inhibitors of  
 CC MDM2/p53 binding. They may also be used to purify binding partners  
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
 CC cancer and leukaemia patients and for treatment or prevention of disease  
 CC involving p53/MDM2 interactions, especially tumours and viral infections.  
 CC The peptides can be administered nasally, rectally, orally or by  
 CC injection. By interfering with MDM2/p53 interaction, the peptides can

CC activate p53 function and accumulation in normal cells. The peptides  
 CC which mimic the MDM2 binding site in p53, have a significantly greater  
 CC blocking activity compared with wild-type p53  
 XX  
 SQ Sequence 12 AA;  
 AAW37170 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..  
 Found using 'claim36' (zara371.key)

1 MPRFMDYWEGLN  
 3 11

-----  
 1 match found in sequence:  
 aaw37172 : Human oncogenic protein MDM2 binding peptide 3.  
 (from "claim36ags.pep")  
 TOIG of: aaw37172 Check: 9428 From: 1 to: 15

ID AAW37172 standard; peptide; 15 AA.  
 XX  
 AC AAW37172;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE Human oncogenic protein MDM2 binding peptide 3.  
 XX  
 KM MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 XX tumour; diagnosis; binding; viral infection.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9801467-A2.  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 04-JUL-1997; 97WO-EP003549.  
 XX  
 PR 05-JUL-1996; 96GB-00014197.  
 XX  
 PR 07-APR-1997; 97GB-00007041.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 XX  
 DR WPI; 1998-100996/09.  
 XX  
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.  
 XX  
 PS Disclosure; Page 4; 45pp; English.  
 XX  
 CC This peptide is capable of binding to an oncogenic protein MDM2  
 CC (especially human MDM2). The MDM2 binding peptides can specifically  
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can  
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type  
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify  
 CC molecules that bind to MDM2 and to identify and design inhibitors of  
 CC MDM2/p53 binding. They may also be used to purify binding partners  
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
 CC cancer and leukaemia patients and for treatment or prevention of disease  
 CC involving p53/MDM2 interactions, especially tumours and viral infections.  
 CC The peptides can be administered nasally, rectally, orally or by  
 CC injection. By interfering with MDM2/p53 interaction, the peptides can  
 CC activate p53 function and accumulation in normal cells. The peptides  
 CC which mimic the MDM2 binding site in p53, have a significantly greater  
 CC blocking activity compared with wild-type p53

SQ Sequence 15 AA;

AAW37172 Length: 15 October 13, 2004 13:39 Type: P Check: 9428 ..  
Found using 'claim36' (zara371.key)1 |-----|  
PRPALVFADYWTLY  
6 14

-----

1 match found in sequence:

aaw37179 ; Human oncogenic protein MDM2 binding peptide derivative 7.  
(from "claim36ags.pep")

TOIG of: aaw37179 check: 3427 from: 1 to: 9

ID AAW37179 standard; peptide; 9 AA.

XX AAW37179;

XX 20-JUL-1998 (first entry)

XX Human oncogenic protein MDM2 binding peptide derivative 7.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;

XX tumour; diagnosis; binding; viral infection.

XX Synthetic.

XX Homo sapiens.

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Pickesley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
XX useful in, e.g. diagnosis and treatment of cancer and viral infections  
XX and identifying binding agents.

XX Disclosure; Page 8; 45pp; English.

XX This peptide is capable of binding to an oncogenic protein MDM2

XX (especially human MDM2). The MDM2 binding peptides can specifically

XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro

XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can

XX induce growth arrest or apoptosis in tumour cells comprising a wild-type

XX p53 and non-elevated levels of MDM2. The peptides may be used to identify

XX molecules that bind to MDM2 and to identify and design inhibitors of

XX MDM2/p53 binding. They may also be used to purify binding partners

XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

XX cancer and leukaemia patients and for treatment or prevention of disease

XX involving p53/MDM2 interactions, especially tumours and viral infections.

XX The peptides can be administered nasally, rectally, orally or by

XX injection. By interfering with MDM2/p53 interaction, the peptides can

XX activate p53 function and accumulation in normal cells. The peptides

XX which mimic the MDM2 binding site in p53, have a significantly greater

XX blocking activity compared with wild-type p53

XX Sequence 9 AA;

AAW37179 Length: 9 October 13, 2004 13:39 Type: P Check: 3427 ..  
Found using 'claim36' (zara371.key)1 |-----|  
RFMDYWEGL  
1 9

-----

1 match found in sequence:

aaw37182 ; Human oncogenic protein MDM2 binding N-acetylated peptide derivative  
(from "claim36ags.pep")

TOIG of: aaw37182 check: 5993 from: 1 to: 12

ID AAW37182 standard; peptide; 12 AA.

XX AAW37182;

XX 20-JUL-1998 (first entry)

XX Human oncogenic protein MDM2 binding N-acetylated peptide derivative 1.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;

XX tumour; diagnosis; binding; viral infection.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

XX Modified-site 12 /note= "C-terminal amide"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Pickesley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
XX useful in, e.g. diagnosis and treatment of cancer and viral infections  
XX and identifying binding agents.

XX Example 1; Page 18; 45pp; English.

XX This is a N-acetylated peptide derivative capable of binding to a human

XX oncogenic protein MDM2. The MDM2 binding peptides can specifically

XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro

XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can

XX induce growth arrest or apoptosis in tumour cells comprising a wild-type

XX p53 and non-elevated levels of MDM2. The peptides may be used to identify

XX molecules that bind to MDM2 and to identify and design inhibitors of

XX MDM2/p53 binding. They may also be used to purify binding partners

XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

XX cancer and leukaemia patients and for treatment or prevention of disease

XX involving p53/MDM2 interactions, especially tumours and viral infections.

XX The peptides can be administered nasally, rectally, orally or by

XX injection. By interfering with MDM2/p53 interaction, the peptides can

XX activate p53 function and accumulation in normal cells. The peptides

XX which mimic the MDM2 binding site in p53, have a significantly greater

XX blocking activity compared with wild-type p53

XX Sequence 12 AA;

AAW37182 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..  
Found using 'claim36' (zara371.key)

1 |-----|  
TCGPAFTHWATF  
4 12

# 1 match found in sequence:

aaaw37183 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative  
(from "claim36ags-pep")  
TOIG of: aaw37183 check: 5978 from: 1 to: 12

ID AAW37183 standard; peptide; 12 AA.

XX AAW37183;

XX 20-JUL-1998 (first entry)

DE Human oncogenic protein MDM2 binding N-acylated peptide derivative 2.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;

KW tumour; diagnosis; binding; viral infection.

XX Synthetic.

OS Homo sapiens.

XX Key

FT Modified-site 1 Location/Qualifiers

FT Modified-site 12 /note= "N-terminal acetyl"

FT Modified-site 12 /note= "C-terminal amide"

XX MO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Pickslay S, Hochkeppel H;

PI Garcia-Echeverria C, Chene P, Furet P;

XX MPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -

PT useful in, e.g. diagnosis and treatment of cancer and viral infections

XX and identifying binding agents.

XX Example 1; Page 19; 45pp; English.

XX This is a N-acylated peptide derivative capable of binding to a human

CC oncogenic protein MDM2. The MDM2 binding peptides can specifically

CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro

CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can

CC induce growth arrest or apoptosis in tumour cells comprising a wild-type

CC p53 and non-elevated levels of MDM2. The peptides may be used to identify

CC molecules that bind to MDM2 and to identify and design inhibitors of

CC MDM2/p53 binding. They may also be used to purify binding partners

CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

CC cancer and leukaemia patients and for treatment or prevention of disease

CC involving p53/MDM2 interactions, especially tumours and viral infections.

CC The peptides can be administered nasally, rectally, orally or by

CC injection. By interfering with MDM2/p53 interaction, the peptides can

CC activate p53 function and accumulation in normal cells. The peptides

CC which mimic the MDM2 binding site in p53, have a significantly greater

XX blocking activity compared with wild-type p53

SQ Sequence 12 AA;

AAW37183 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..  
Found using 'claim36' (zara371.key)

1 |-----|  
MPRFMDWEGIAN  
3 11

# 1 match found in sequence:

aaaw37191 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative  
(from "claim36ags-pep")  
TOIG of: aaw37191 check: 6151 from: 1 to: 12

ID AAW37191 standard; peptide; 12 AA.

XX AAW37191;

XX 20-JUL-1998 (first entry)

DE Human oncogenic protein MDM2 binding N-acylated peptide derivative 10.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;

KW tumour; diagnosis; binding; viral infection.

XX Synthetic.

OS Homo sapiens.

XX Key

FT Modified-site 1 Location/Qualifiers

FT Modified-site 12 /note= "N-terminal acetyl"

FT Modified-site 12 /note= "C-terminal amide"

XX MO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Pickslay S, Hochkeppel H;

PI Garcia-Echeverria C, Chene P, Furet P;

XX MPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -

PT useful in, e.g. diagnosis and treatment of cancer and viral infections

XX and identifying binding agents.

XX Example 1; Page 19; 45pp; English.

XX This is a N-acylated peptide derivative capable of binding to a human

CC oncogenic protein MDM2. The MDM2 binding peptides can specifically

CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro

CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can

CC induce growth arrest or apoptosis in tumour cells comprising a wild-type

CC p53 and non-elevated levels of MDM2. The peptides may be used to identify

CC molecules that bind to MDM2 and to identify and design inhibitors of

CC MDM2/p53 binding. They may also be used to purify binding partners

CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

CC cancer and leukaemia patients and for treatment or prevention of disease

CC involving p53/MDM2 interactions, especially tumours and viral infections.

CC The peptides can be administered nasally, rectally, orally or by

CC injection. By interfering with MDM2/p53 interaction, the peptides can

CC activate p53 function and accumulation in normal cells. The peptides

CC which mimic the MDM2 binding site in p53, have a significantly greater

CC blocking activity compared with wild-type p53  
 XX Sequence 12 AA;  
 SQ

AAW37191 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 VONFIDYWTQOF  
 3 11

1 match found in sequence:

aaw37192 ; Human oncogenic protein MDM2 binding N-acetylated peptide derivative  
 (from "claim36ags.pep")  
 TOIG of: aaw37192 check: 9093 from: 1 to: 15

ID AAW37192 standard; peptide, 15 AA.

XX AAW37192;

XX 20-JUL-1998 (first entry)

XX Human oncogenic protein MDM2 binding N-acetylated peptide derivative 11.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 XX tumour; diagnosis; binding; viral infection.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

XX Modified-site 15 /note= "C-terminal amide"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Plicksley S, Hochkeppel H;  
 XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 XX useful in, e.g. diagnosis and treatment of cancer and viral infections  
 XX and identifying binding agents.

XX Example 1; Page 19; 45pp; English.

XX This is a N-acetylated peptide derivative capable of binding to a human  
 XX oncogenic protein MDM2. The MDM2 binding peptides can specifically

XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
 XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can

XX induce growth arrest or apoptosis in tumour cells comprising a wild-type  
 XX p53 and non-elevated levels of MDM2. The peptides may be used to identify

XX molecules that bind to MDM2 and to identify and design inhibitors of  
 XX MDM2/p53 binding. They may also be used to purify binding partners

XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
 XX cancer and leukaemia patients and for treatment or prevention of disease

XX involving p53/MDM2 interactions, especially tumours and viral infections.

XX The peptides can be administered nasally, rectally, orally or by  
 XX injection. By interfering with MDM2/p53 interaction, the peptides can

CC activate p53 function and accumulation in normal cells. The peptides  
 CC which mimic the MDM2 binding site in p53, have a significantly greater  
 CC blocking activity compared with wild-type p53  
 XX

SQ Sequence 15 AA;

AAW37192 Length: 15 October 13, 2004 13:39 Type: P Check: 9093 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 IDRAPFFRDHWFATV  
 6 14

1 match found in sequence:

aaw37193 ; Human oncogenic protein MDM2 binding N-acetylated peptide derivative  
 (from "claim36ags.pep")  
 TOIG of: aaw37193 check: 9428 from: 1 to: 15

ID AAW37193 standard; peptide, 15 AA.

XX AAW37193;

XX 20-JUL-1998 (first entry)

XX Human oncogenic protein MDM2 binding N-acetylated peptide derivative 12.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 XX tumour; diagnosis; binding; viral infection.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

XX Modified-site 15 /note= "C-terminal amide"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Plicksley S, Hochkeppel H;  
 XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 XX useful in, e.g. diagnosis and treatment of cancer and viral infections  
 XX and identifying binding agents.

XX Example 1; Page 19; 45pp; English.

XX This is a N-acetylated peptide derivative capable of binding to a human  
 XX oncogenic protein MDM2. The MDM2 binding peptides can specifically

XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
 XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can

XX induce growth arrest or apoptosis in tumour cells comprising a wild-type  
 XX p53 and non-elevated levels of MDM2. The peptides may be used to identify

XX molecules that bind to MDM2 and to identify and design inhibitors of  
 XX MDM2/p53 binding. They may also be used to purify binding partners

XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
 XX cancer and leukaemia patients and for treatment or prevention of disease

XX involving p53/MDM2 interactions, especially tumours and viral infections.



CC The peptides can be administered nasally, rectally, orally or by  
 CC injection. By interfering with MDM2/p53 interaction, the peptides can  
 CC activate p53 function and accumulation in normal cells. The peptides  
 CC which mimic the MDM2 binding site in p53, have a significantly greater  
 CC blocking activity compared with wild-type p53  
 CC  
 SQ Sequence 15 AA;

AAW37193 Length: 15 October 13, 2004 13:39 Type: P Check: 9428 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 PRPALVFPADYWTLY  
 6 14

1 match found in sequence:  
 aaw37194 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative  
 (from "claim36ags.pep")  
 TOIG of: aaw37194 Check: 8833 from: 1 to: 15

ID AAW37194 standard; peptide; 15 AA.  
 XX  
 AC AAW37194;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE Human oncogenic protein MDM2 binding N-acylated peptide derivative 13.  
 XX  
 DE MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 XX tumour; diagnosis; binding; viral infection.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 15 /note= "C-terminal amide"  
 FT  
 PN WO9801467-A2.  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 04-JUL-1997; 97WO-EP003549.  
 XX  
 PR 05-JUL-1996; 96GB-00014197.  
 PR 07-APR-1997; 97GB-00007041.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Lane D, Boettger V, Boettger A, Picketsley S, Hochkeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 XX  
 DR WPI; 1998-100996/09.  
 XX  
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.  
 XX  
 PS Example 1; Page 19; 45pp; English.  
 XX  
 CC This is a N-acylated peptide derivative capable of binding to a human  
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically  
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can  
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type  
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify  
 CC molecules that bind to MDM2 and to identify and design inhibitors of  
 CC MDM2/p53 binding. They may also be used to purify binding partners  
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

CC cancer and leukaemia patients and for treatment or prevention of disease  
 CC involving p53/MDM2 interactions, especially tumours and viral infections.  
 CC The peptides can be administered nasally, rectally, orally or by  
 CC injection. By interfering with MDM2/p53 interaction, the peptides can  
 CC activate p53 function and accumulation in normal cells. The peptides  
 CC which mimic the MDM2 binding site in p53, have a significantly greater  
 CC blocking activity compared with wild-type p53  
 CC  
 SQ Sequence 15 AA;

AAW37194 Length: 15 October 13, 2004 13:39 Type: P Check: 8833 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 PAFSRFWSDSL SAGAH  
 2 10

1 match found in sequence:  
 aaw37195 ; Human oncogenic protein MDM2 binding C-amidated peptide derivative  
 (from "claim36ags.pep")  
 TOIG of: aaw37195 Check: 5993 from: 1 to: 12

ID AAW37195 standard; peptide; 12 AA.  
 XX  
 AC AAW37195;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE Human oncogenic protein MDM2 binding C-amidated peptide derivative 1.  
 XX  
 DE MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 XX tumour; diagnosis; binding; viral infection.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 12 /note= "C-terminal amide"  
 FT  
 PN WO9801467-A2.  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 04-JUL-1997; 97WO-EP003549.  
 XX  
 PR 05-JUL-1996; 96GB-00014197.  
 PR 07-APR-1997; 97GB-00007041.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Lane D, Boettger V, Boettger A, Picketsley S, Hochkeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 XX  
 DR WPI; 1998-100996/09.  
 XX  
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.  
 XX  
 PS Example 1; Page 20; 45pp; English.  
 XX  
 CC This is a C-amidated peptide derivative capable of binding to a human  
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically  
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can  
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type  
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify  
 CC molecules that bind to MDM2 and to identify and design inhibitors of  
 CC MDM2/p53 binding. They may also be used to purify binding partners  
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

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CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX
SQ Sequence 12 AA;
AAW37195 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..
Found using 'claim36' (zara371.key)

1 -----|
1 TGPAPTHYWTAP 12
4

-----|
1 match found in sequence:
aaw37196 ; Human oncogenic protein MDM2 binding C-amidated peptide derivative
(from "claim36ags.pep")
TOIG of: aaw37196 check: 5978 from: 1 to: 12

ID AAW37196 standard; peptide; 12 AA.
XX
XX AAW37196;
AC
XX
XX 20-JUL-1998 (first entry)
DT
XX
DE Human oncogenic protein MDM2 binding C-amidated peptide derivative 2.
XX
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 12
XX FT /note= "C-terminal amide"
XX FT
XX PN WO9801467-A2.
XX
XX PD 15-JAN-1998.
XX
XX PF 04-JUL-1997; 97WO-EP003549.
XX
XX PR 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX PA (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX PI Garcia-Echeverria C, Chene P, Furet P;
XX
XX DR WPI; 1998-100996/09.
XX
XX PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX PT useful in, e.g. diagnosis and treatment of cancer and viral infections
XX PT and identifying binding agents.
XX
XX PS Example 1; Page 20; 45pp; English.
XX
XX This is a C-amidated peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of
XX MDM2/p53 binding. They may also be used to purify binding partners
XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

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CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX
SQ Sequence 12 AA;
AAW37196 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..
Found using 'claim36' (zara371.key)

1 -----|
1 MPRFMDYBGLN 11
3

-----|
1 match found in sequence:
aaw37204 ; Human oncogenic protein MDM2 binding biotinylated peptide derivativ
(from "claim36ags.pep")
TOIG of: aaw37204 check: 1571 from: 1 to: 28

ID AAW37204 standard; peptide; 28 AA.
XX
XX AAW37204;
AC
XX
XX 20-JUL-1998 (first entry)
DT
XX
DE Human oncogenic protein MDM2 binding biotinylated peptide derivative 4.
XX
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection; biotinylation.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX FT /note= "biotinylated"
XX FT 28
XX FT Modified-site
XX FT /note= "C-terminal amide"
XX FT
XX PN WO9801467-A2.
XX
XX PD 15-JAN-1998.
XX
XX PF 04-JUL-1997; 97WO-EP003549.
XX
XX PR 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX PA (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX PI Garcia-Echeverria C, Chene P, Furet P;
XX
XX DR WPI; 1998-100996/09.
XX
XX PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX PT useful in, e.g. diagnosis and treatment of cancer and viral infections
XX PT and identifying binding agents.
XX
XX PS Example 3; Page 21; 45pp; English.
XX
XX This is a biotinylated peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of

```

CC MDM2/p53 binding. They may also be used to purify binding partners  
CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
CC cancer and leukaemia patients and for treatment or prevention of disease  
CC involving p53/MDM2 interactions, especially tumours and viral infections.  
CC The peptides can be administered nasally, rectally, orally or by  
CC injection. By interfering with MDM2/p53 interaction, the peptides can  
CC activate p53 function and accumulation in normal cells. The peptides  
CC which mimic the MDM2 binding site in p53, have a significantly greater  
CC blocking activity compared with wild-type p53

Sequence 28 AA;

AAW37204 Length: 28 October 13, 2004 13:39 Type: P Check: 1571 ..  
Found using 'claim36' (zara371.key)

1 |-----|  
4 SMPRFMDYEGLNRIQIKWFOHMKMKK  
12

1 match found in sequence:  
aaw37205 ; Human oncogenic protein MDM2 binding biotinylated peptide derivativ  
(from "claim36agrs.pep")  
TOIG of: aaw37205 check: 8233 from: 1 to: 31

ID AAW37205 standard; peptide; 31 AA.

AC AAW37205;

DT 20-JUL-1998 (first entry)

DE Human oncogenic protein MDM2 binding biotinylated peptide derivative 5.

KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
tumour; diagnosis; binding; viral infection; biotinylation.

OS Synthetic.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 17 /label= bAla

FT Modified-site 30 /note= "beta-Alanine"

FT Modified-site 31 /label= bAla

FT Modified-site 31 /note= "beta-Alanine"

FT Modified-site 31 /note= "biotinylated"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Pickaley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX MPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
XX useful in, e.g. diagnosis and treatment of cancer and viral infections  
XX and identifying binding agents.  
XX Example 3; Page 21; 45pp; English.

XX This is a biotinylated peptide derivative capable of binding to a human  
CC oncogenic protein MDM2. The MDM2 binding peptides can specifically  
CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can  
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type  
CC p53 and non-elevated levels of MDM2. The peptides may be used to identify  
CC molecules that bind to MDM2 and to identify and design inhibitors of  
CC MDM2/p53 binding. They may also be used to purify binding partners  
CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
CC cancer and leukaemia patients and for treatment or prevention of disease  
CC involving p53/MDM2 interactions, especially tumours and viral infections.  
CC The peptides can be administered nasally, rectally, orally or by  
CC injection. By interfering with MDM2/p53 interaction, the peptides can  
CC activate p53 function and accumulation in normal cells. The peptides  
CC which mimic the MDM2 binding site in p53, have a significantly greater  
CC blocking activity compared with wild-type p53

Sequence 31 AA;

AAW37205 Length: 31 October 13, 2004 13:39 Type: P Check: 8233 ..  
Found using 'claim36' (zara371.key)

1 |-----|  
20 AAVALPAAVLALALAPMPRFMDYEGLNK  
28

1 match found in sequence:

aaw37216 ; Human oncogenic protein MDM2 binding peptide derivative 9.  
(from "claim36agrs.pep")  
TOIG of: aaw37216 check: 3427 from: 1 to: 9

ID AAW37216 standard; peptide; 9 AA.

AC AAW37216;

DT 20-JUL-1998 (first entry)

DE Human oncogenic protein MDM2 binding peptide derivative 9.

KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
tumour; diagnosis; binding; viral infection.

OS Synthetic.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 9 /note= "C-terminal amide"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Pickaley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX MPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
XX useful in, e.g. diagnosis and treatment of cancer and viral infections  
XX and identifying binding agents.

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XX Example 6; Page 26; 45pp; English.
PS This is a MDM2 binding peptide derivative capable of binding to a human
CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC molecules that bind to MDM2 and to identify and design inhibitors of
CC MDM2/p53 binding. They may also be used to purify binding partners
CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC cancer and leukemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
SQ Sequence 9 AA;
AAW37216 Length: 9 October 13, 2004 13:39 Type: P Check: 3427 ..
Found using 'claim36' (zara371.key)
1 -----|
1 RFDMDYWEGL
9
1 match found in sequence:
aaw37220; MDM2 binding peptide unique phage insert sequence 1.
(from "claim36agr.pep")
TOIG of: aaw37220 check: 5978 from: 1 to: 12
ID AAW37220 standard; peptide; 12 AA.
XX
XX AAW37220;
XX
XX 20-JUL-1998 (first entry)
XX
XX MDM2 binding peptide unique phage insert sequence 1.
XX
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection; phage insert.
XX
XX Homo sapiens.
XX
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Pickesley S, Hochkeppel H;
XX Garcia-Scheverria C, Chene P, Furet P;
XX
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Example 8; Page 30; 45pp; English.
XX This is a unique phage insert sequence of the MDM2 binding peptide
XX identified by phage display. The MDM2 binding peptides and their

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CC derivatives are capable of binding to the human oncogenic protein MDM2.
CC These peptides can specifically inhibit or block the binding of MDM2 to
CC the human p53 protein, in vitro or in vivo. Inhibiting the interaction
CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The
CC peptides may be used to identify molecules that bind to MDM2 and to
CC identify and design inhibitors of MDM2/p53 binding. They may also be used
CC to purify binding partners especially MDM2, diagnose disease by measuring
CC levels of MDM2 in blood of cancer and leukemia patients and for
CC treatment or prevention of disease involving p53/MDM2 interactions,
CC especially tumours and viral infections. The peptides can be administered
CC nasally, rectally, orally or by injection. By interfering with MDM2/p53
CC interaction, the peptides can activate p53 function and accumulation in
CC normal cells. The peptides which mimic the MDM2 binding site in p53, have
CC a significantly greater blocking activity compared with wild-type p53
SQ Sequence 12 AA;
AAW37220 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..
Found using 'claim36' (zara371.key)
1 -----|
1 MPDFMDYWEGLN
3
11
1 match found in sequence:
aaw37221; MDM2 binding peptide unique phage insert sequence 2.
(from "claim36agr.pep")
TOIG of: aaw37221 check: 6151 from: 1 to: 12
ID AAW37221 standard; peptide; 12 AA.
XX
XX AAW37221;
XX
XX 20-JUL-1998 (first entry)
XX
XX MDM2 binding peptide unique phage insert sequence 2.
XX
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection; phage insert.
XX
XX Homo sapiens.
XX
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Pickesley S, Hochkeppel H;
XX Garcia-Scheverria C, Chene P, Furet P;
XX
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Example 8; Page 30; 45pp; English.
XX This is a unique phage insert sequence of the MDM2 binding peptide
XX identified by phage display. The MDM2 binding peptides and their
XX derivatives are capable of binding to the human oncogenic protein MDM2.
XX These peptides can specifically inhibit or block the binding of MDM2 to
XX the human p53 protein, in vitro or in vivo. Inhibiting the interaction
XX between the p53 and MDM2 can induce growth arrest or apoptosis in tumour

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CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The  
 CC peptides may be used to identify molecules that bind to MDM2 and to  
 CC identify and design inhibitors of MDM2/p53 binding. They may also be used  
 CC to purify binding partners especially MDM2, diagnose disease by measuring  
 CC levels of MDM2 in blood of cancer and leukaemia patients and for  
 CC treatment or prevention of disease involving p53/MDM2 interactions,  
 CC especially tumours and viral infections. The peptides can be administered  
 CC nasally, rectally, orally or by injection. By interfering with MDM2/p53  
 CC interaction, the peptides can activate p53 function and accumulation in  
 CC normal cells. The peptides which mimic the MDM2 binding site in p53, have  
 CC a significantly greater blocking activity compared with wild-type p53  
 CC  
 CC Sequence 12 AA:

AAW37221 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..  
 Found using 'claim36' (zara371.key)

1 -----  
 3 VONFIDYWTQGF  
 11

1 match found in sequence:  
 aaw37222 : MDM2 binding peptide unique phage insert sequence 3.  
 (from "claim36agr-pep")  
 TOIG of: aaw37222 Check: 5993 from: 1 to: 12

ID AAW37222 standard; peptide; 12 AA.  
 AC AAW37222;  
 XX  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE MDM2 binding peptide unique phage insert sequence 3.  
 XX  
 KM MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KM tumour; diagnosis; binding; viral infection; phage insert.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9801467-A2.  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 04-JUL-1997; 97WO-EP003549.  
 XX  
 PR 05-JUL-1996; 96GB-00014197.  
 PR 07-APR-1997; 97GB-00007041.  
 XX  
 XX (NOVS ) NOVARTIS AG.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 PA  
 PI Lane D, Boettger V, Boettger A, Pickasley S, Hochkeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 XX  
 DR WPI; 1998-100996/09.  
 XX  
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.  
 XX  
 XX Example 8; Page 30; 45pp; English.  
 PS  
 CC This is a unique phage insert sequence of the MDM2 binding peptide  
 CC identified by phage display. The MDM2 binding peptides and their  
 CC derivatives are capable of binding to the human oncogenic protein MDM2.  
 CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour  
 CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The  
 CC peptides may be used to identify molecules that bind to MDM2 and to  
 CC identify and design inhibitors of MDM2/p53 binding. They may also be used  
 CC to purify binding partners especially MDM2, diagnose disease by measuring

CC levels of MDM2 in blood of cancer and leukaemia patients and for  
 CC treatment or prevention of disease involving p53/MDM2 interactions,  
 CC especially tumours and viral infections. The peptides can be administered  
 CC nasally, rectally, orally or by injection. By interfering with MDM2/p53  
 CC interaction, the peptides can activate p53 function and accumulation in  
 CC normal cells. The peptides which mimic the MDM2 binding site in p53, have  
 CC a significantly greater blocking activity compared with wild-type p53  
 CC  
 CC Sequence 12 AA:

AAW37222 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..  
 Found using 'claim36' (zara371.key)

1 -----  
 4 TGPAPTHYWTAP  
 12

1 match found in sequence:  
 aaw37223 : MDM2 binding peptide unique phage insert sequence 4.  
 (from "claim36agr-pep")  
 TOIG of: aaw37223 Check: 9093 from: 1 to: 15

ID AAW37223 standard; peptide; 15 AA.  
 AC AAW37223;  
 XX  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE MDM2 binding peptide unique phage insert sequence 4.  
 XX  
 KM MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KM tumour; diagnosis; binding; viral infection; phage insert.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9801467-A2.  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 04-JUL-1997; 97WO-EP003549.  
 XX  
 PR 05-JUL-1996; 96GB-00014197.  
 PR 07-APR-1997; 97GB-00007041.  
 XX  
 XX (NOVS ) NOVARTIS AG.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 PA  
 PI Lane D, Boettger V, Boettger A, Pickasley S, Hochkeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 XX  
 DR WPI; 1998-100996/09.  
 XX  
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.  
 XX  
 XX Example 8; Page 30; 45pp; English.  
 PS  
 CC This is a unique phage insert sequence of the MDM2 binding peptide  
 CC identified by phage display. The MDM2 binding peptides and their  
 CC derivatives are capable of binding to the human oncogenic protein MDM2.  
 CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour  
 CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The  
 CC peptides may be used to identify molecules that bind to MDM2 and to  
 CC identify and design inhibitors of MDM2/p53 binding. They may also be used  
 CC to purify binding partners especially MDM2, diagnose disease by measuring  
 CC levels of MDM2 in blood of cancer and leukaemia patients and for  
 CC treatment or prevention of disease involving p53/MDM2 interactions,  
 CC especially tumours and viral infections. The peptides can be administered  
 CC nasally, rectally, orally or by injection. By interfering with MDM2/p53

CC interaction, the peptides can activate p53 function and accumulation in  
 CC normal cells. The peptides which mimic the MDM2 binding site in p53, have  
 CC a significantly greater blocking activity compared with wild-type p53  
 XX  
 SQ Sequence 15 AA;

AAW37223 Length: 15 October 13, 2004 13:39 Type: P Check: 9093 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 IDRAPFRDHWFFALV  
 6 14

1 match found in sequence:

aaw37224 ; MDM2 binding peptide unique phage insert sequence 5.

(from "claim36ags.pep")  
 TOIG of: aaw37224 Check: 9428 from: 1 to: 15

ID AAW37224 standard; peptide; 15 AA.

XX AAW37224;

XX 20-JUL-1998 (first entry)

XX MDM2 binding peptide unique phage insert sequence 5.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KM tumour; diagnosis; binding; viral infection; phage insert.

XX Homo sapiens.

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

PI Lane D, Boettger V, Boettger A, Pickstley S, Hochkeppel H;

PI Garcia-Echeverria C, Chene P, Furet P;

XX MPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.

PS Example 8; Page 30; 45pp; English.

XX This is a unique phage insert sequence of the MDM2 binding peptide  
 CC identified by phage display. The MDM2 binding peptides and their  
 CC derivatives are capable of binding to the human oncogenic protein MDM2.  
 CC These peptides can specifically inhibit or block the binding of MDM2 to  
 CC the human p53 protein, in vitro or in vivo. Inhibiting the interaction  
 CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour  
 CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The  
 CC peptides may be used to identify molecules that bind to MDM2 and to  
 CC identify and design inhibitors of MDM2/p53 binding. They may also be used  
 CC to purify binding partners especially MDM2, diagnose disease by measuring  
 CC levels of MDM2 in blood of cancer and leukaemia patients and for  
 CC treatment or prevention of disease involving p53/MDM2 interactions,  
 CC especially tumours and viral infections. The peptides can be administered  
 CC nasally, rectally, orally or by injection. By interfering with MDM2/p53  
 CC interaction, the peptides can activate p53 function and accumulation in  
 CC normal cells. The peptides which mimic the MDM2 binding site in p53, have  
 CC a significantly greater blocking activity compared with wild-type p53  
 XX

SQ Sequence 15 AA;

AAW37224 Length: 15 October 13, 2004 13:39 Type: P Check: 9428 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 PRPALVFADYWETLY  
 6 14

1 match found in sequence:

aaw37225 ; MDM2 binding peptide unique phage insert sequence 6.

(from "claim36ags.pep")  
 TOIG of: aaw37225 Check: 8833 from: 1 to: 15

ID AAW37225 standard; peptide; 15 AA.

XX AAW37225;

XX 20-JUL-1998 (first entry)

XX MDM2 binding peptide unique phage insert sequence 6.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KM tumour; diagnosis; binding; viral infection; phage insert.

XX Homo sapiens.

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

PI Lane D, Boettger V, Boettger A, Pickstley S, Hochkeppel H;

PI Garcia-Echeverria C, Chene P, Furet P;

XX MPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
 PT and identifying binding agents.

PS Example 8; Page 30; 45pp; English.

XX This is a unique phage insert sequence of the MDM2 binding peptide  
 CC identified by phage display. The MDM2 binding peptides and their  
 CC derivatives are capable of binding to the human oncogenic protein MDM2.  
 CC These peptides can specifically inhibit or block the binding of MDM2 to  
 CC the human p53 protein, in vitro or in vivo. Inhibiting the interaction  
 CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour  
 CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The  
 CC peptides may be used to identify molecules that bind to MDM2 and to  
 CC identify and design inhibitors of MDM2/p53 binding. They may also be used  
 CC to purify binding partners especially MDM2, diagnose disease by measuring  
 CC levels of MDM2 in blood of cancer and leukaemia patients and for  
 CC treatment or prevention of disease involving p53/MDM2 interactions,  
 CC especially tumours and viral infections. The peptides can be administered  
 CC nasally, rectally, orally or by injection. By interfering with MDM2/p53  
 CC interaction, the peptides can activate p53 function and accumulation in  
 CC normal cells. The peptides which mimic the MDM2 binding site in p53, have  
 CC a significantly greater blocking activity compared with wild-type p53  
 XX

SQ Sequence 15 AA;

AAW37225 Length: 15 October 13, 2004 13:39 Type: P Check: 8833 ..  
 Found using 'claim36' (zara371.key)

1 PAFSRFMSDLSAGAH  
2 10

1 match found in sequence:  
AAW82320 ; p53 homologue TIP 12/1 peptide.  
(from "claim36ags.pep")  
TOIG of: AAW82320 Check: 4400 from: 1 to: 19

ID AAW82320 standard; peptide; 19 AA.  
XX  
AC AAW82320;  
XX  
DT 22-FEB-1999 (first entry)  
XX  
DE p53 homologue TIP 12/1 peptide.  
XX  
KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.  
XX  
OS Synthetic.  
XX  
PN WO9847525-A1.  
XX  
PD 29-OCT-1998.  
XX  
PF 20-APR-1998; 98WO-GB001144.  
XX  
PR 22-APR-1997; 97GB-00080892.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Lane DP;  
XX  
DR WPI; 1998-609975/51.  
XX  
PT New agents which inhibit interaction of p53 and mdm2 - useful for  
PT activating p53, e.g. for treating cancer; viral conditions or other  
PT conditions associated with non functional p53 or mdm2.  
XX  
PS Disclosure; Fig 1; 52pp; English.  
XX  
CC This sequence is a peptide homologue of a region of p53 which binds to  
CC mdm2. This peptide is used in the construction of a novel agent capable  
CC of disrupting the binding of p53 and mdm2 or inhibiting the production of  
CC mdm2 in a population of cells. This agent is also used in the preparation  
CC of a therapeutic for activating p53, where the population of cells do not  
CC overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the  
CC binding of mdm2 to p53 allows levels of p53 to increase by reducing the  
CC clearance of p53 by mdm2, and can be used to activate p53 function. The  
CC agents for use in therapeutics for activating p53 can be used for the  
CC treatment of cancer, viral conditions or other conditions associated with  
CC non-functional p53  
XX  
SQ Sequence 19 AA;

AAW82320 Length: 19 October 13, 2004 13:39 Type: P Check: 4400 ..  
Found using 'claim36' (zara371.key)

1 PPLSMRPFMDYMEGLNENG  
7 15

1 match found in sequence:  
AAW82322 ; p53 homologue TIP 12/1 peptide.  
(from "claim36ags.pep")  
TOIG of: AAW82322 Check: 4400 from: 1 to: 19

ID AAW82322 standard; peptide; 19 AA.  
XX  
AC AAW82322;

XX 22-FEB-1999 (first entry)  
DT  
XX  
DE p53 homologue TIP 12/1 peptide.  
XX  
KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.  
XX  
OS Synthetic.  
XX  
PN WO9847525-A1.  
XX  
PD 29-OCT-1998.  
XX  
PF 20-APR-1998; 98WO-GB001144.  
XX  
PR 22-APR-1997; 97GB-00080892.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Lane DP;  
XX  
DR WPI; 1998-609975/51.  
XX  
PT New substance with a mdm2 binding domain and coupling partner - useful  
PT for stabilising in cells without an efficient mdm2-mediated degradation  
PT pathway.  
XX  
PS Disclosure; Fig 1; 52pp; English.

XX  
CC This sequence is a peptide homologue of a region of p53 which binds to  
CC mdm2. This peptide is used in the construction of a novel agent capable  
CC of disrupting the binding of p53 and mdm2 or inhibiting the production of  
CC mdm2 in a population of cells. This agent is also used in the preparation  
CC of a therapeutic for activating p53, where the population of cells do not  
CC overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the  
CC binding of mdm2 to p53 allows levels of p53 to increase by reducing the  
CC clearance of p53 by mdm2, and can be used to activate p53 function. The  
CC agents for use in therapeutics for activating p53 can be used for the  
CC treatment of cancer, viral conditions or other conditions associated with  
CC non-functional p53  
XX  
SQ Sequence 19 AA;

AAW82322 Length: 19 October 13, 2004 13:39 Type: P Check: 4400 ..  
Found using 'claim36' (zara371.key)

1 PPLSMRPFMDYMEGLNENG  
7 15

1 match found in sequence:  
ABB65993 ; Drosophila melanogaster polypeptide SEQ ID NO 24771.  
(from "claim36ags.pep")  
TOIG of: ABB65993 Check: 1097 from: 1 to: 1075

ID ABB65993 standard; protein; 1075 AA.  
XX  
AC ABB65993;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 24771.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX

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PF 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI MPI; 2001-656860/75.
DR N-PDDB; ABL10096.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 24771; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1075 AA;
SQ
AB65993 Length: 1075 October 13, 2004 13:39 Type: P Check: 1097 ..
Found using 'claim36' (zara371.key)
...
451 VPKDICQSGNTNITWCPCLCDWCMFMDLKETCNVAKVTYLIDNPSTVFPAVMSFWATLF
-----|
501 509
511 LELMKRYSAEITHRMDLTGRDVHEHPRPOYLARLEHIPPTRDYVTNI
...
-----|
1 match found in sequence:
abb73174; Mdm/hdm antagonist peptide SEQ ID NO:135.
(from "claim36ags.pep")
TOIG of: abb73174 Check: 5978 from: 1 to: 12
ID ABB73174 standard; peptide; 12 AA.
XX
XX ABB73174;
AC
XX
XX 05-APR-2002 (first entry)
DT
XX
XX Mdm/hdm antagonist peptide SEQ ID NO:135.
DE
XX
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
XX TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
XX TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
XX cytostatic; antineumatic; antiarthritic; haemostatic; dermatological;
KW antianemic; anorectic; antifertility; haemostatic; dermatological;
XX neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
XX sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
XX Fanconi's syndrome.
OS Homo sapiens.
OS Synthetic.

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XX
XX WO200183525-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US014310.
PF
XX
XX 03-MAY-2000; 2000US-00563286.
PR
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudus JW;
PI MPI; 2002-130313/17.
DR
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Claim 39; Page 53; 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antineumatic, antiarthritic, antidiabetic, dermatological and
CC antianemic, anorectic, antifertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. AB872403 to AB873426 and AB835695 to AB835777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
XX Sequence 12 AA;
SQ
AB873174 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..
Found using 'claim36' (zara371.key)
1 -----|
1 MPRFMDYMEGLN
3 11
-----|
1 match found in sequence:
abb73175; Mdm/hdm antagonist peptide SEQ ID NO:136.
(from "claim36ags.pep")
TOIG of: abb73175 Check: 6151 from: 1 to: 12
ID ABB73175 standard; peptide; 12 AA.
XX
XX ABB73175;
AC
XX
XX 05-APR-2002 (first entry)
DT
XX
XX Mdm/hdm antagonist peptide SEQ ID NO:136.
DE
XX
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
XX TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
XX TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
XX cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;
KW

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KM antihaemic; anorectic; antifertility; haemostatic; dermatological;  
 KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KM cancer; rheumatoid arthritis; diabetic; retinopathy; infertility; obesity;  
 KM sleep disorder; neurological degenerative disease; anaemia;  
 KM thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
 KM Fanconi's syndrome.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200183525-A2.  
 PD 08-NOV-2001.  
 PF 02-MAY-2001; 2001WO-US014310.  
 PR 03-MAY-2000; 2000US-00563286.  
 PA (AMGE-) AMGEN INC.  
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
 DR WPI; 2002-130313/17.  
 PT Novel vehicle-peptide molecule or its multimers useful for treating  
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility.  
 XX  
 PS Claim 39; Page 53; 176pp; English.  
 XX  
 CC The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antidiabetic, ophthalmological,  
 CC antinaeemic, anorectic, antifertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
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 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
 CC mimetic compounds are useful for treating disorders characterised by low  
 CC red blood cell levels such as anaemia. The EPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention  
 CC  
 XX  
 SQ Sequence 12 AA;  
 ABB73175 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..  
 Found using 'claim36' (zara371.key)  
 1  
 3  
 11  
 VQNFIDYWTQOF  
 -----  
 1 match found in sequence:  
 ABB73176; Mdm/hdm antagonist peptide SEQ ID NO:137.  
 (from "claim36ags.dep")  
 TOIG of: ABB73176 check: 5993 from: 1 to: 12  
 ID ABB73176 standard; peptide; 12 AA.  
 XX  
 AC ABB73176;  
 XX  
 DT 05-APR-2002 (first entry)

XX  
 DE Mdm/hdm antagonist peptide SEQ ID NO:137.  
 XX  
 KM Modified peptide; mimetic; Fe domain; fusion; immunoglobulin G; IgG; EPO;  
 KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KM TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TGF-  
 KM TPO mimetic peptide; EPO mimetic peptide; EGF; VEGF antagonist;  
 KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KM cytostatic; antirheumatic; antidiabetic; ophthalmological;  
 KM antihaemic; anorectic; antifertility; haemostatic; dermatological;  
 KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 KM sleep disorder; neurological degenerative disease; anaemia;  
 KM thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
 KM Fanconi's syndrome.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200183525-A2.  
 PD 08-NOV-2001.  
 PF 02-MAY-2001; 2001WO-US014310.  
 PR 03-MAY-2000; 2000US-00563286.  
 PA (AMGE-) AMGEN INC.  
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
 DR WPI; 2002-130313/17.  
 PT Novel vehicle-peptide molecule or its multimers useful for treating  
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility.  
 XX  
 PS Claim 39; Page 53; 176pp; English.  
 XX  
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 CC cytostatic, antirheumatic, antidiabetic, ophthalmological,  
 CC antinaeemic, anorectic, antifertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
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 CC interest, as a part of diagnostic kit to detect the presence of their  
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 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
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 CC mimetic compounds are useful for treating disorders characterised by low  
 CC red blood cell levels such as anaemia. The EPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention  
 CC  
 XX  
 SQ Sequence 12 AA;  
 ABB73176 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..  
 Found using 'claim36' (zara371.key)  
 1  
 4  
 12  
 TGPATHTHWATP  
 -----  
 1 match found in sequence:

abb73177 ; Mdm/hdm antagonist peptide SEQ ID NO:138.  
(from "claim36ags.pep")  
TOIG of: abb73177 check: 9093 from: 1 to: 15

ID ABB73177 standard; peptide; 15 AA.

XX ABB73177;

DT 05-APR-2002 (first entry)

DE Mdm/hdm antagonist peptide SEQ ID NO:138.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;  
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TGF;  
KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;  
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
KW cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;  
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;  
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
KW sleep disorder; neurological degenerative disease; anaemia;  
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
KW Fanconi's syndrome.

XX Homo sapiens.  
OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

PT Novel vehicle-peptide molecule or its multimers useful for treating  
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
PT diabetic retinopathy, obesity, sleep disorders and infertility.

PS Claim 39; Page 53; 176pp; English.

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CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
CC cytostatic, antineumatic, antiarthritic, antidiabetic, ophthalmological,  
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and  
CC neuroprotective activities. (I) can be used as a therapeutic or  
CC prophylactic agent as well as for screening purposes. (I) is useful for  
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CC protein of interest, for identifying normal or abnormal proteins of  
CC interest, as a part of diagnostic kit to detect the presence of their  
CC proteins of interest in a biological sample. Additionally, (I) is useful  
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CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
CC mimetic compounds are useful for treating disorders characterised by low  
CC red blood cell levels such as anaemia. The TPO-mimetic comprising  
CC compounds are useful for treating conditions that involve an existing  
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB35695 to ABB35777  
CC represent amino acid and nucleic acid sequences used in the  
CC exemplification of the present invention

XX Sequence 15 AA;

ABB73177 Length: 15 October 13, 2004 13:39 Type: P Check: 9093  
Found using 'claim36' (zaxa371.key)

1 IDRAPFRDHFALV  
6 14

-----  
1 match found in sequence:

abb73178 ; Mdm/hdm antagonist peptide SEQ ID NO:139.  
(from "claim36ags.pep")  
TOIG of: abb73178 check: 9428 from: 1 to: 15

ID ABB73178 standard; peptide; 15 AA.

XX ABB73178;

DT 05-APR-2002 (first entry)

DE Mdm/hdm antagonist peptide SEQ ID NO:139.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;  
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TGF;  
KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;  
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
KW cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;  
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;  
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
KW sleep disorder; neurological degenerative disease; anaemia;  
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
KW Fanconi's syndrome.

XX Homo sapiens.  
OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

PT Novel vehicle-peptide molecule or its multimers useful for treating  
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
PT diabetic retinopathy, obesity, sleep disorders and infertility.

PS Claim 39; Page 53; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its  
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
CC cytostatic, antineumatic, antiarthritic, antidiabetic, ophthalmological,  
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and  
CC neuroprotective activities. (I) can be used as a therapeutic or  
CC prophylactic agent as well as for screening purposes. (I) is useful for  
CC diagnosing diseases characterised by dysfunction of their associated  
CC protein of interest, for identifying normal or abnormal proteins of  
CC interest, as a part of diagnostic kit to detect the presence of their  
CC proteins of interest in a biological sample. Additionally, (I) is useful  
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
CC mimetic compounds are useful for treating disorders characterised by low  
CC red blood cell levels such as anaemia. The TPO-mimetic comprising  
CC compounds are useful for treating conditions that involve an existing

CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 15 AA:  
 ABB73178 Length: 15 October 13, 2004 13:39 Type: P Check: 9428 ..  
 Found using 'claim36' (zara371.key)  
 1 -----  
 PRAVYFADWERTLY  
 6 14  
 1 match found in sequence:  
 ABB73179; Mdm/hdm antagonist peptide SEQ ID NO:140.  
 (from "claim36ags.pep")  
 TOIG of: ABB73179 Check: 8833 from: 1 to: 15  
 ID ABB73179 standard; peptide; 15 AA.  
 XX  
 AC ABB73179;  
 XX  
 DT 05-APR-2002 (first entry)  
 XX  
 DE Mdm/hdm antagonist peptide SEQ ID NO:140.  
 XX  
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;  
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;  
 KW TPO mimetic peptide; EPO mimetic peptide; EBP; VEGF antagonist;  
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KW cytostatic; antirheumatic; antidiabetic; ophthalmological;  
 KW antianemic; anorectic; antifertility; haemostatic; dermatological;  
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KW cancer; rheumatoid arthritis; diabetic retinopathy; obesity;  
 KW sleep disorder; neurological degenerative disease; anaemia;  
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;  
 KW Fanconi's syndrome.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200183525-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014310.  
 XX  
 PR 03-MAY-2000; 2000US-00563286.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudaa JM;  
 XX  
 DR WPI; 2002-130313/17.  
 XX  
 PT Novel vehicle-peptide molecule or its multimers useful for treating  
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility.  
 XX  
 PS Claim 39; Page 53; 176pp; English.  
 XX  
 CC The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antidiabetic, antidiabetic, ophthalmological,  
 CC antianemic, anorectic, antifertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated

CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
 CC mimetic compounds are useful for treating disorders characterised by low  
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 15 AA:  
 ABB73179 Length: 15 October 13, 2004 13:39 Type: P Check: 8833 ..  
 Found using 'claim36' (zara371.key)  
 1 -----  
 PAFSRFMSDLASAGAH  
 2 10  
 1 match found in sequence:  
 ABB92234; Herbicidally active polypeptide SEQ ID NO 1445.  
 (from "claim36ags.pep")  
 TOIG of: ABB92234 Check: 9732 from: 1 to: 440  
 ID ABB92234 standard; protein; 440 AA.  
 XX  
 AC ABB92234;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 1445.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 OS  
 PN WO200210210-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 28-AUG-2001; 2001WO-EP009892.  
 XX  
 PR 28-AUG-2001; 2001WO-EP009892.  
 XX  
 PA (PARB ) BAYER AG.  
 XX  
 PI Tietjen K, Weidler M;  
 XX  
 DR WPI; 2002-269010/31.  
 XX  
 PT Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms.  
 XX  
 PS Claim 5; SEQ ID NO 1445; 261pp + Sequence Listing; English.  
 XX  
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
 CC for herbicidally active compounds, comprising aligning and comparing  
 CC nucleic acid or amino acid sequences from plant with nucleic acid or  
 CC amino acid sequences from non-plant organisms using suitable search  
 CC parameters, where plant sequences having an E-value greater by a factor  
 CC of 3 than the E-value of most similar non-plant sequences are selected.  
 CC The polypeptides or nucleic acids encoding them are useful for  
 CC identifying modulators. The identified modulators are useful as  
 CC herbicides

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XX      SQ      Sequence 440 AA;
ABB92234 Length: 440   October 13, 2004 13:39   Type: P   Check: 9732   ..
Found using 'claim36' (zara371.key)
...
350      KTEYKESLPAPENNNDLYKGKIMCVGNNTCDPIRGSPCCQKPDLTVLHASYAFSSYWAQFR
                                         |-----|
                                         400      408
410      KIGGTCSFNGLATQTITKDPBSYGRCEPPSVTL

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1 match found in sequence:
abb92409 ; Herbicidally active polypeptide SEQ ID NO 1620.
(from "claim36ags.pep")
TOIG of: abb92409 check: 2170 from: 1 to: 476

ID      ABB92409 standard; protein; 476 AA.
XX
AC      ABB92409;
XX
DT      31-MAY-2002 (first entry)
XX
DE      Herbicidally active polypeptide SEQ ID NO 1620.
XX
KM      Herbicidal; plant; agriculture; herbicide.
XX
OS      Arabidopsis thaliana.
XX
PN      WO200210210-A2.
XX
PD      07-FEB-2002.
XX
PF      28-AUG-2001; 2001WO-EP009892.
XX
PR      28-AUG-2001; 2001WO-EP009892.
XX
PA      (FARB ) BAYER AG.
XX
PI      Tietjen K, Weidler M;
XX
DR      WPI; 2002-269010/31.
XX
PT      Identifying plant target proteins for herbicidally active compounds,
PT      comprising aligning and comparing nucleic acid or amino acid sequences
PT      from plant with nucleic acid or amino acid sequences from non-plant
PT      organisms.
XX
PS      Claim 5; SEQ ID NO 1620; 261pp + Sequence Listing; English.
XX
CC      The invention relates to identifying target proteins (ABB90790-ABB94016)
CC      for herbicidally active compounds, comprising aligning and comparing
CC      nucleic acid or amino acid sequences from plant with nucleic acid or
CC      amino acid sequences from non-plant organisms using suitable search
CC      parameters, where plant sequences having an E-value greater by a factor
CC      of 3 than the E-value of most similar non-plant sequences are selected.
CC      The polypeptides or nucleic acids encoding them are useful for
CC      identifying modulators. The identified modulators are useful as
CC      herbicides
XX
SQ      Sequence 476 AA;
ABB92409 Length: 476   October 13, 2004 13:39   Type: P   Check: 2170   ..
Found using 'claim36' (zara371.key)
...
386      VMCVAVDGADEALGQALNFCGRSNATCAALAPGGECAVPTVTWTHASVAFSSYWAQFR
                                         |-----|
                                         436      444

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446      NOSQCYFNGLARETTTPNGNERCKPPSVTL
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1 match found in sequence:
adb61841 ; Peptide Seq ID81 related to inhibitors of apoptosis.
(from "claim36ags.pep")
TOIG of: adb61841 check: 3739 from: 1 to: 29

ID      ADB61841 standard; peptide; 29 AA.
XX
AC      ADB61841;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Peptide Seq ID81 related to inhibitors of apoptosis.
XX
KM      baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM      apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM      autoimmune disorder; neurodegenerative disease; apoptotic response;
KM      systemic lupus erythematosus; multiple sclerosis; viral infection;
KM      herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM      H1AP1; CIAP2; H1AP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KM      caspase-9; cytoskeletal; neoplasm; leukemia; colon carcinoma;
KM      cervical cancer; uterine cancer; testicular cancer;
KM      small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM      Wilms' tumour.
XX
OS      Unidentified.
XX
PN      WO2003040172-A2.
XX
PD      15-MAY-2003.
XX
PF      12-NOV-2002; 2002WO-CA001738.
XX
PR      09-NOV-2001; 2001US-033230P.
XX
PR      08-APR-2002; 2002US-0370934P.
XX
PA      (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI      Boudreault A, Korneljuk RG, La Casse E, Liston P;
XX
DR      WPI; 2003-513532/48.
XX
PT      Polypeptide capable of forming a complex with a polypeptide comprising a
PT      baculovirus inhibitor of apoptosis repeat domain useful for treating
PT      cancer and other neoplasms.
XX
PS      Disclosure; Page 13; 53pp; English.
XX
CC      This invention relates to a substantially pure polypeptide having a
CC      length of less than 100 amino acids and capable of forming a complex with
CC      a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC      (BIR) domain. The apoptosis pathway is known to play a critical role in
CC      embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC      and neurodegenerative diseases. The failure of the apoptotic response has
CC      been implicated in the development of cancer, autoimmune disorders (for
CC      example systemic lupus erythematosus and multiple sclerosis) and viral
CC      infections (including herpes virus, poxvirus and adenovirus. The
CC      inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC      more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1AP1
CC      (CIAP2) and H1AP2 (CIAP1) all possess three BIR domains and carboxy
CC      terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC      -9 which are proteases involved in the initiation of apoptosis. Compounds
CC      which inhibit the activity of IAPs may therefore have cytostatic activity
CC      through the enhancement of apoptosis. The polypeptides of the invention
CC      are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC      may be useful for the treatment of cancer and other neoplasms, such as
CC      leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC      cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC      and Wilms' tumour, and for enhancing apoptosis. The present sequence is
CC      that of a peptide which is suggested as a possible peptide for fusing to

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CC the IAP protein BIR domain-binding peptides of the invention.  
 XX  
 SQ Sequence 29 AA;

ADB61841 Length: 29 October 13, 2004 13:39 Type: P Check: 3739 ..  
 Found using 'claim36' (zara371.key)

1 |-----|  
 3 MPRFMDYEGLNQIKIMFQNERRMKKKK  
 11

-- Search Statistics --

Times:	CPU	Total Elapsed
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Number of sequences searched:		50
Number of sequence hits:		50
Number of separate matches:		50
Number of sequence hits saved:		0

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